

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:49:56 ; Search time 39 Seconds

(without alignments)  
249.177 Million cell updates/sec

Title: US-10-678-588a-8

Perfect score: 459

Sequence: 1 REQDRYLPANISRIKMKAL.....FEDYIEPLKYLXXYREXEG 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417.5	91.0	179	2 S22820	transcription fact
2	407.5	88.8	228	2 T45874	transcription fact
3	405.5	88.3	138	2 E84810	hypothetical prote
4	400.5	87.3	161	2 G71407	transcription fact
5	393.5	85.7	178	2 A84788	probable CCAAT-box
6	376.5	82.0	215	2 F84508	probable CCAAT-box
7	373.5	73.5	160	2 S24469	transcription fact
8	337.5	73.5	205	2 S22817	transcription fact
9	337.5	73.5	207	2 F38245	transcription fact
10	337.5	73.5	207	2 A23625	transcription fact
11	336.5	72.0	186	2 JC6080	transcription fact
12	330.5	72.0	209	2 S22818	transcription fact
13	325.5	70.9	160	2 G84919	transcription fact
14	308.5	67.2	208	2 G86352	probable CCAAT-box
15	288.5	62.9	144	1 A28123	protein T26P17.20
16	280.5	61.1	139	2 C86222	transcription fact
17	280.5	61.1	205	2 S51565	hypothetical prote
18	271.5	59.2	116	2 S42744	transcription fact
19	255.5	55.7	403	2 E88021	transcription fact
20	230	50.1	122	2 S22819	protein M10D9.4 [1
21	144.5	31.5	159	2 T50504	transcription fact
22	142.5	31.0	159	2 S53582	DR1-like protein -
23	137	29.8	175	2 JC5365	TATA-binding prote
24	136	29.6	176	2 A43320	TBP-binding repres
25	119	25.9	161	2 T40194	TATA-binding prote
26	117	25.5	275	2 C84673	probable transcrip
27	94.5	20.6	184	2 T22529	hypothetical prote
28	85.5	18.6	210	2 T40369	probable dna bindi
29	79.5	17.3	72	2 A69292	archaeal histone A

30	74.5	16.2	69	2 A35959	archaeal histone H
31	74.5	16.2	146	2 S69594	hypothetical prote
32	74	16.1	137	2 T34387	hypothetical prote
33	72.5	15.8	67	2 A64321	archaeal histone -
34	72.5	15.6	67	2 D64416	archaeal histone -
35	71.5	15.6	69	2 A47036	histone-related pr
36	71.5	15.6	69	2 T48848	histone Hmf1 limpo
37	70.5	15.4	752	2 A98111	maltoedextrin phosp
38	70.5	15.4	752	2 D95246	glycogen phosphory
39	69	15.0	2178	2 S29237	calcium channel pr
40	69	15.0	2222	2 A37490	calcium channel pr
41	69	15.0	2251	2 B54972	voltage-dependent
42	69	15.0	2259	2 S29236	voltage-dependent
43	69	15.0	2270	2 A54972	calcium channel pr
44	69	15.0	2272	2 C54972	voltage-dependent
45	68.5	14.9	697	2 F84646	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S22820 transcription factor NF-Y, CCAAT-binding, chain B - maize

N:Alternate names: CCAAT-box DNA-binding protein

C:Species: Zea mays (maize)

C>Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 09-Jul-2004

C/Accession: S22820

R:Li, X.Y.; Mantovani, R.; van Huijdedijnen, R.H.; Andre, I.; Benoist, C.; Mathis, D.

Nucleic Acids Res. 20, 1087-1091, 1992

A:Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.

A:Reference number: S22816; MUID:92195809; PMID:11549471

A/Accession: S22820

A/Molecule type: mRNA

A/Residues: 1-179 <LIX>

A/Cross-references: UNIPROT:P25209; EMBL:X59714

C:Superfamily: transcription factor HAP3

C/Keywords: DNA binding; transcription regulation

F/30-119/Domain: DNA binding #status predicted <DNA>

Query Match 91.0%; Score 417.5; DB 2; Length 179;  
Best Local Similarity 83.2%; Pred. No. 3.2e-47;  
Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 REQDRYLPANISRIKMKALPNKXXXXXXIAKDAKXTXQCVSFFISFTSASXKC 60

Db 30 REQDRFLPANISRIKMKALIPANGK-----IAKDAKXTXQCVSFFISFTSASDKC 82

QY 61 QXERKRTINGDDILMMATIGFEDYIEPLKYLXXYREXEG 101

Db 83 QXERKRTINGDDILMMATIGFEDYIEPLKYLXXYREXEG 123

##### RESULT 2

T45874 transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana

N:Alternate names: protein PAP2.40

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004

C/Accession: T45874

R:Blöcker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quétier, F.; Salanoubat, M.

submitted to the Protein Sequence Database, January 2000

A/Reference number: Z23016

A/Accession: T45874

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-228 <BL0>

A/Cross-references: UNIPROT:Q9LPT3; EMBL:AL132966

A/Experimental source: cultivar Columbia; BAC clone PAP12

C/Genetics:

A/Map position: 3

A/Insertions: 75/2; 116/3; 120/3; 145/3; 164/3; 179/3; 213/1

A/Note: PAP2.40

Query Match 88.8%; Score 407.5; DB 2; Length 228;  
Best Local Similarity 80.2%; Pred. No. 8,6e-46;  
Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60  
DB 28 REODRFLPIANISIRIMKALPXNGK-----IAKDAKTXQECVSEFISFITSASXKC 80

QY 61 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 101  
DB 81 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 121

RESULT 3  
B84810  
hypothetical protein At2g38880 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: B84810  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: B84810  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-138 <STO>  
A/Cross-references: UNIPROT:Q9SLG0; GB:AE002093; NID:G3928076; PIDN:AC79602.1; GSPDB:GN  
C/Genetics:  
A/Map position: 2  
A/Map position: 2  
C/Superfamily: transcription factor HAP3

Query Match 88.3%; Score 405.5; DB 2; Length 138;  
Best Local Similarity 80.0%; Pred. No. 9.1e-46;  
Matches 80; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60  
DB 20 REODRFLPIANISIRIMKALPXNGK-----IAKDAKTXQECVSEFISFITSASXKC 72

QY 61 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 100  
DB 73 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 112

RESULT 4  
G71407  
transcription factor, CCAAT-binding, chain A - Arabidopsis thaliana  
N/Alternate names: protein DL3310W  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
A/Variety: Columbia  
C/Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: G71407  
R/Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
P.; Medler, H.; Medler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel  
avannah, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998  
A/Authors: Mueller-Auer, S.; Silve, M.; James, R.; Montfort, A.; Pons, A.; Pulgomenech  
erhoff, A.; Moore, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rehnman, S.; And  
C.; Chludzinski, N.  
A/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
A/Reference number: A71400; MUID:98121113; PMID:9461215  
A/Accession: G71407  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-161 <BEV>  
A/Cross-references: UNIPROT:O23310; GB:Z97336; NID:G2244788; PIDN:CAB10233.1; PID:G22448  
C/Genetics:  
A/Map position: 4COP9-4G3845

A/Note: DL3310W  
C/Superfamily: transcription factor HAP3  
C/Keywords: DNA binding; transcription regulation  
P/20-109/Domain: DNA binding #status predicted <DNA>

Query Match 87.3%; Score 400.5; DB 2; Length 161;  
Best Local Similarity 78.2%; Pred. No. 4.9e-45;  
Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60  
DB 20 REODRFLPIANISIRIMKALPXNGK-----IAKDAKTXQECVSEFISFITSASXKC 72

QY 61 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 101  
DB 73 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 113

RESULT 5  
A84788  
probable CCAAT-box binding transcription factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: A84788  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: A84788  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-178 <STO>  
A/Cross-references: UNIPROT:Q9ZQC3; GB:AE002093; NID:G4371295; PIDN:AD18153.1; GSPDB:GN  
C/Genetics:  
A/Map position: 2

Query Match 85.7%; Score 393.5; DB 2; Length 178;  
Best Local Similarity 78.0%; Pred. No. 4.5e-44;  
Matches 78; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60  
DB 29 REODRFLPIANISIRIMKALPXNGK-----IAKDAKTXQECVSEFISFITSASXKC 81

QY 61 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 100  
DB 82 QXERKTINGDDLMMAMATGFEEDYIEPLKYLXXYREXG 121

RESULT 6  
F84508  
probable CCAAT-box binding transcription factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: F84508  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: F84508  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-215 <STO>  
A/Cross-references: UNIPROT:Q9SLT9; GB:AE002093; NID:G4558662; PIDN:AD22680.1; GSPDB:GN  
C/Genetics:  
A/Map position: 2

Query Match 82.0%; Score 376.5; DB 2; Length 215;  
Best Local Similarity 70.3%; Pred. No. 9.6e-42;  
Matches 71; Conservative 10; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYPIANISIRIMKALPXNGKXXXXXXIXAKAKXTYQECVSEFISFTSEASXKC 60  
Db 35 KEDRPIPIANVAGIMKALPXNGK-----IKDAKECVQECVSEFISFTSEASXKC 87

Qy 61 QXERKTINGDDLLMAMATGFEEDYIBPLKYYLXXYREXG 101  
Db 88 QXERKTINGDDLLMAMATGFEEDYVAPLKYLLCKYRDTGG 128

RESULT 7  
S24469  
transcription factor NF-Y, CCAAT-binding, chain B - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C/Accession: S24469  
R/Benoist, C.  
submitted to the EMBL Data Library, January 1992  
A/Reference number: S24469  
A/Accession: S24469  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-180 <BEN>  
A/Cross-references: EMBL:X59713; NID:g63690; PIDN:CAA42233.1; PID:g63691  
C/Superfamily: transcription factor HAP3  
C/Keywords: DNA binding; transcription regulation  
F/51-140/Domain: DNA binding #status predicted <DNA>

Query Match 73.5%; Score 337.5; DB 2; Length 180;  
Best Local Similarity 67.3%; Pred. No. 1.1e-36;  
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYPIANISIRIMKALPXNGKXXXXXXIXAKAKXTYQECVSEFISFTSEASXKC 60  
Db 51 REODIYPIANVARIKNAIPQTK-----IAKDAKECVQECVSEFISFTSEASERC 103

Qy 61 QXERKTINGDDLLMAMATGFEEDYIBPLKYYLXXYRE 98  
Db 104 HQERKTINGEDLLFAMSTIGFDSYVPLKYLQKPRE 141

RESULT 8  
S22817  
transcription factor NF-Y, CCAAT-binding, chain B - human  
N/Alternate names: CAAAT-box DNA-binding protein  
C/Species: Homo sapiens (man)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C/Accession: S22817  
R/Li, X.Y.; Mantovan, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis, D.  
Nucleic Acids Res. 20, 1087-1091, 1992  
A/Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.  
A/Reference number: S22816; MUID:92195809; PMID:1549471  
A/Accession: S22817  
A/Molecule type: mRNA  
A/Residues: 1-205 <LIX>  
A/Cross-references: EMBL:X59710; NID:g35049; PIDN:CAA42230.1; PID:g35050  
C/Superfamily: transcription factor HAP3  
C/Keywords: DNA binding; transcription regulation  
F/51-140/Domain: DNA binding #status predicted <DNA>

Query Match 73.5%; Score 337.5; DB 2; Length 205;  
Best Local Similarity 67.3%; Pred. No. 1.2e-36;  
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYPIANISIRIMKALPXNGKXXXXXXIXAKAKXTYQECVSEFISFTSEASXKC 60  
Db 51 REODIYPIANVARIKNAIPQTK-----IAKDAKECVQECVSEFISFTSEASERC 103

Qy 61 QXERKTINGDDLLMAMATGFEEDYIBPLKYYLXXYRE 98  
Db 104 HQERKTINGEDLLFAMSTIGFDSYVPLKYLQKPRE 141

Db 104 HQERKTINGEDLLFAMSTIGFDSYVPLKYLQKPRE 141

RESULT 9  
F38245  
transcription factor NF-Y, CCAAT-binding, chain B - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C/Accession: F38245  
R/Li, X.Y.; Hooft van Hujsduijnen, R.; Mantovan, R.; Benoist, C.; Mathis, D.  
J. Biol. Chem. 267, 8984-8990, 1992  
A/Title: Intron-exon organization of the NF-Y genes. Tissue-specific splicing modifies a  
A/Reference number: A38245; MUID:92250488; PMID:1577736  
A/Accession: F38245  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-207 <LIA>  
A/Cross-references: UNIPROT:P22569; GB:M6215  
R/Hooft van Hujsduijnen, R.; Li, X.Y.; Black, D.; Mathis, H.; Benoist, C.; Mathis, D.  
EMBO J. 9, 3119-3127, 1990  
A/Title: Co-evolution from yeast to mouse: cDNA cloning of the two NF-Y (CP-1/CBF) subun  
A/Reference number: S12044; MUID:91006004; PMID:1698608  
A/Accession: S12045  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-207 <HOO>  
A/Cross-references: GB:X55316; NID:g53362; PIDN:CAA39024.1; PID:g53363  
C/Superfamily: transcription factor HAP3  
C/Keywords: alternative splicing; DNA binding; transcription regulation

Query Match 73.5%; Score 337.5; DB 2; Length 207;  
Best Local Similarity 67.3%; Pred. No. 1.2e-36;  
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYPIANISIRIMKALPXNGKXXXXXXIXAKAKXTYQECVSEFISFTSEASXKC 60  
Db 53 REODIYPIANVARIKNAIPQTK-----IAKDAKECVQECVSEFISFTSEASERC 105

Qy 61 QXERKTINGDDLLMAMATGFEEDYIBPLKYYLXXYRE 98  
Db 106 HQERKTINGEDLLFAMSTIGFDSYVPLKYLQKPRE 143

RESULT 10  
A23692  
transcription factor, CCAAT-binding, chain A1 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004  
C/Accession: A23692  
R/Vuorio, T.; Maitly, S.N.; de Crombrughe, B.  
J. Biol. Chem. 266, 22480-22486, 1990  
A/Title: Purification and molecular cloning of the "A" chain of a rat heteromeric CCAAT-  
A/Reference number: A23692; MUID:91093096; PMID:2266139  
A/Accession: A23692  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-207 <VVO>  
A/Cross-references: UNIPROT:P22569; GB:M55045; GB:J05701; NID:g203352; PIDN:AAA40887.1;  
C/Superfamily: transcription factor HAP3  
C/Keywords: alternative splicing; DNA binding; transcription regulation  
F/51-142/Domain: DNA binding #status predicted <DNA>

Query Match 73.5%; Score 337.5; DB 2; Length 207;  
Best Local Similarity 67.3%; Pred. No. 1.2e-36;  
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYPIANISIRIMKALPXNGKXXXXXXIXAKAKXTYQECVSEFISFTSEASXKC 60  
Db 53 REODIYPIANVARIKNAIPQTK-----IAKDAKECVQECVSEFISFTSEASERC 105

Qy 61 QXERKTINGDDLLMAMATGFEEDYIBPLKYYLXXYRE 98  
Db 106 HQERKTINGEDLLFAMSTIGFDSYVPLKYLQKPRE 143

## RESULT 11

transcription factor HAP3 - *Emeticella nidulans*  
C/Species: *Emeticella nidulans*, *Aspergillus nidulans*  
C/Date: 21-Jan-1997 #sequence\_revision 21-Jan-1997 #text\_change 09-Jul-2004  
C/Accession: J06080  
R/Papagiamopoulos, P.; Andrianopoulos, A.; Sharp, J.A.; Davis, M.A.; Hynes, M.J.  
Mol. Gen. Genet. 251, 412-421, 1996  
A/Title: The hapC gene of *Aspergillus nidulans* is involved in the expression of CCAAT-cc  
A/Reference number: J06080; MUID:96285564; PMID:8709944  
A/Accession: J06080  
A/Molecule type: mRNA  
A/Residues: 1-186 <PAP>  
A/Cross-references: UNIPROT:Q00735; GB:U05341; NID:g1017715; PIDN:AA049411.1; PID:g10177  
C/Genetics:  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 53/1; 90/1; 132/3  
A/Intons: 53/1; 90/1; 132/3  
C/Superfamily: transcription factor HAP3  
F/42-131/Domain: DNA binding #status predicted <DNA>

Query Match 73.3%; Score 336.5; DB 2; Length 186;  
Best Local Similarity 66.0%; Pred. No. 1.5e-36;  
Matches 66; Conservative 13; Mismatches 14; Indels 7; Gaps 1;

Qy 1 REDRYIPINISIRIMKALPXNGKXXXXXXIAKDAKTXQRCVSEFISFITSASXKC 60  
Db 42 KEODRWLPINAVNIRIMKALPENK-----IAKEAKECQECVSEFISFITSASEKC 94  
Qy 61 QXERKTINGDDLLAMATLGFEDYIEPLKYLXXYREX 100  
Db 95 QXERKTINGDDILFAMSTLGFENYARALKITLYSKYRETO 134

## RESULT 12

transcription factor NF-Y, CCAAT-binding, chain B - see lamprey  
N/Alternate names: CCAAT-box DNA-binding protein  
C/Species: *Petromyzon marinus* (sea lamprey)  
C/Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 09-Jul-2004  
C/Accession: S22818; S78116  
R/Li, X.Y.; Mantovani, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Machie, D.  
Nucleic Acids Res. 20, 1087-1091, 1992  
A/Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.  
A/Reference number: S22818; MUID:92195809; PMID:1549471  
A/Molecule type: mRNA  
A/Residues: 1-209 <LIX>  
A/Cross-references: UNIPROT:P25210; EMBL:X59712  
R/Benoist, C.  
Submitted to the EMBL Data Library, January 1992  
A/Reference number: S78116  
A/Accession: S78116  
A/Molecule type: mRNA  
A/Residues: 1-110, 'R', 112-209 <BEN>  
A/Cross-references: EMBL:X55712; NID:964217; PIDN:CAA42232.1; PID:964218  
C/Superfamily: transcription factor HAP3  
C/Keywords: DNA binding; transcription regulation  
F/54-143/Domain: DNA binding #status predicted <DNA>

Query Match 72.0%; Score 330.5; DB 2; Length 209;  
Best Local Similarity 66.3%; Pred. No. 1e-35;  
Matches 65; Conservative 12; Mismatches 14; Indels 7; Gaps 1;

Qy 1 REDRYIPINISIRIMKALPXNGKXXXXXXIAKDAKTXQRCVSEFISFITSASXKC 60  
Db 54 REDQIYIPINAVNIRIMKTSISGK-----IAKDAECQECVSEFISFITSASBRC 106  
Qy 61 QXERKTINGDDLLAMATLGFEDYIEPLKYLXXYRE 98  
Db 107 HQEKRTINGDDILFAMSTLGFDSYVEPLKQYLQYRE 144

## RESULT 13

probable CCAAT-box binding transcription factor [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: G84919  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: G84919  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-160 <STO>  
A/Cross-references: UNIPROT:O82248; GB:AE002093; NID:g3738293; PIDN:AA063635.1; GSPDB:GN  
C/Genetics:  
A/Status: preliminary  
A/Map position: 2  
C/Superfamily: transcription factor HAP3

Query Match 70.9%; Score 325.5; DB 2; Length 160;  
Best Local Similarity 62.4%; Pred. No. 3.5e-35;  
Matches 63; Conservative 9; Mismatches 22; Indels 7; Gaps 1;

Qy 1 REDRYIPINISIRIMKALPXNGKXXXXXXIAKDAKTXQRCVSEFISFITSASXKC 60  
Db 50 KEODRLPINAVNIRIMKNIIPANAK-----VSKAKETMORCVSEFISFIVGEASDKC 102  
Qy 61 QXERKTINGDDLLAMATLGFEDYIEPLKYLXXYREX 101  
Db 103 HKEKRTINGDDICWAPANLGFDDYAAQLKYLHRRYVLEG 143

## RESULT 14

protein T2EF17.20 [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: G86352  
R/Theodoglia, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Comol, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luvo, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: G86352  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-208 <STO>  
A/Cross-references: UNIPROT:Q9SFD8; GB:AE005172; NID:9655738; PIDN:AA016537.1; GSPDB:GN  
C/Genetics:  
A/Map position: 1

Query Match 67.2%; Score 308.5; DB 2; Length 208;  
Best Local Similarity 56.0%; Pred. No. 8e-33;  
Matches 56; Conservative 20; Mismatches 17; Indels 7; Gaps 1;

Qy 1 REDRYIPINISIRIMKALPXNGKXXXXXXIAKDAKTXQRCVSEFISFITSASXKC 60  
Db 28 REDQIYIPINAVNIRIMKTPSHAK-----ISDPAKETIQECVSEFISFIVGEANBRC 80  
Qy 61 QXERKTINGDDLLAMATLGFEDYIEPLKYLXXYREX 100

Db 81 QREQRKTTAEDILWAMSKLGFDNYVDP LTVFINRRYREIE 120

## RESULT 15

A28123

transcription factor HAP3 - yeast (*Saccharomyces cerevisiae*)

N: Alternate names: protein YBL021c; protein YBL0441

C/Species: *Saccharomyces cerevisiae*

C:\Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004

C:\Accesslon: A28123; S43937; S45755

R;Hahn, S.; Pinkham, J.; Wei, R.; Miller, R.; Guarente, L.

Mol. Cell. Biol. 8, 655-663, 1988

A;Title: The HAP3 regulatory locus of *Saccharomyces cerevisiae* encodes divergent overlap

A:Reference number: A93110; MUID:88174707; PMID:28327322

A; Accession: A28123

A;Molecule type: DNA

A;Residues: 1-144 &lt;HAH&gt;

A:Cross-references: UNIPROT:P13434; EMBL:M20318; NID:g577522; PIDN:AAA53538.1; PID:g1716

R; van Dyck, L.; Pearce, D.A.; Sherman, F.

J. Biol. Chem. 269, 238-242, 1994

**A/Title:** PIM1 encodes a mitochondrial ATP-dependent protease that is required for mitochondria

A;Reference number: S43937; MUID:94103216; PMID:82768000

A;Accession: S43937

A: molecule type: DNA

A;Residues: 1-144 &lt;VAN&gt;

A/Cross-references: EMBL:X74544; NID:g453234; PIDN:CMA52633.1; PID:g453235

R; Goffeau, A.; Joniaux, J. L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.

submitted to the Protein Sequence Database, August 1994.

A;Reference number: S45745

**A;Accession: S45755**

A: Molecule type: DNA

A;Residues: 1-144 &lt;GOF&gt;

A; Cross-references: EMBL:Z35782; NID:g536016; PIDN:CAA84840.1; PID:g536017; GSPDB:GN000001

**C;Genetics:**

A; Gene: SGD:HAP3; MIPS:YBL021C

A; Cross-references: SGD:S0000117; MIPS:YBL021c

A;Map position: 2L

C; Superfamily: transcription factor HAP3

**C/Key words:** DNA binding; nucleus; transcription regulation

F;36-125/Domain: DNA binding #status predicted <DNA>

Query Match	62.9%; Score 288.5; DB 1; Length 144;
-------------	---------------------------------------

Best Local Similarity 55.0%; Pred. No. 2.3e-30;

Matches 55; Conservative 18; Mismatches 20; Indels 7; Gaps 1;

1 REQDRYLPANISRMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISPITSEASXKC 600

[illegible]

Search completed: November 17, 2005, 08:59:36  
Job time : 40 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:49:05 ; Search time 164 Seconds  
(without alignments)  
238.188 Million cell updates/sec

Title: US-10-678-588A-8  
Perfect score: 459  
Sequence: 1 REDDRRLPLANISRIKMKAL.....FEDYIEPLKYLXXYREXEG 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	423.5	92.3	160	AD142339	Ad142339 Plant tra
2	423.5	92.3	160	AD16959	Ad16959 Plant pol
3	423.5	92.3	173	AD063706	Ad063706 Transcript
4	423.5	92.3	173	AD16957	Ad16957 Plant pol
5	423.5	92.3	174	AD063718	Ad063718 Transcript
6	423.5	92.3	174	AD063704	Ad063704 Transcript
7	423.5	92.3	174	AD16958	Ad16958 Plant pol
8	417.5	91.0	178	ABG70264	ABG70264 LEC-1-rel
9	417.5	91.0	178	ABR40821	ABR40821 Zea mays
10	417.5	91.0	178	AD142322	AD142322 Plant tra
11	417.5	91.0	179	AD142323	AD142323 Plant tra
12	417.5	91.0	290	ADCC3665	ADCC3665 Polypepti
13	414.5	90.3	141	3 AAG04651	3 AAG04651 Arabidops
14	414.5	90.3	141	7 ADB37175	7 ADB37175 Plant yle
15	414.5	90.3	141	7 ADF50740	7 ADF50740 Thale cre
16	414.5	90.3	141	8 AD141625	8 AD141625 Plant tra
17	414.5	90.3	141	8 AD003369	8 AD003369 Thalecres
18	414.5	90.3	141	8 ADO03292	8 ADO03292 Transcript
19	414.5	90.3	141	8 AD16960	8 AD16960 Plant pol
20	414.5	90.3	182	ABG70259	ABG70259 LEC-1-rel
21	414.5	90.3	182	ABR40742	ABR40742 Triticum
22	413.5	90.1	177	5 ABG70249	5 ABG70249 LEC-1-rel
23	413.5	90.1	177	6 ABR40732	6 ABR40732 Eucalyptu
24	413.5	90.1	177	7 ADC23649	7 ADC23649 Polypepti
25	412.5	89.9	215	8 AD142328	8 AD142328 Plant tra

26	409.5	89.2	174	5 ABG70248	ABG70248 LEC-1-rel
27	409.5	89.2	174	6 ABR40731	ABR40731 Momordica
28	409.5	89.2	174	7 ADC23647	ADC23647 Polypepti
29	407.5	88.8	162	5 ABR40256	ABR40256 Polypepti
30	407.5	88.8	162	6 ABR40739	ABR40739 Glycine m
31	407.5	88.8	162	7 ADC23663	ADC23663 Polypepti
32	407.5	88.8	185	8 AD142329	AD142329 Plant tra
33	407.5	88.8	185	8 AD063668	AD063668 Transcript
34	407.5	88.8	185	8 AD16965	AD16965 Plant pol
35	407.5	88.8	228	5 ABR40823	ABR40823 LEC-1-rel
36	407.5	88.8	228	6 ABR40826	ABR40826 Arabidops
37	407.5	88.8	228	7 ADC23666	ADC23666 Polypepti
38	407.5	88.8	228	8 AD143709	AD143709 Plant tra
39	407.5	88.8	228	8 AD003497	AD003497 Thalecres
40	407.5	88.8	228	8 AD063035	AD063035 Transcript
41	407.5	88.8	228	8 AD16962	AD16962 Plant pol
42	406.5	88.6	164	5 ABR40250	ABR40250 LEC-1-rel
43	406.5	88.6	164	6 ABR40733	ABR40733 Zea mays
44	406.5	88.6	164	7 ADC23651	ADC23651 Polypepti
45	406.5	88.6	164	7 ADC23651	ADC23651 Polypepti

# ALIGNMENTS

RESULT 1	AD142339	standard; protein; 160 AA.
ID	AD142339	standard; protein; 160 AA.
XX	AD142339	
AC	AD142339	
XX	AD142339	
DT	22-APR-2004	(first entry)
XX	22-APR-2004	(first entry)
DE	Plant transcription factor #319.	
XX		
KW	transgenic; plant; enhanced tolerance to abiotic stress;	
KW	glycophosphate tolerance; hormone sensitivity; disease resistance;	
KW	sugar sensing; flowering; flower structure; stem bifurcation;	
KW	branching pattern; apical dominance; trichome; stem morphology;	
KW	root growth; root hair; seed development; cell proliferation;	
KW	cell differentiation; premature senescence; necrosis; plant size;	
KW	leaf morphology; seed morphology; seed biochemistry; root anthocyanin;	
KW	plant anthocyanin; light response; shade avoidance; bioinformatic;	
KW	transcription factor; gene; ds.	
XX		
OS	Glycine max.	
XX		
PN	US2004019927-A1.	
XX		
PD	29-JAN-2004.	
XX		
PF	25-FEB-2003; 2003US-00374780.	
XX		
PR	18-APR-2001; 2001US-00637944.	
XX		
PA	(SHER/) SHERMAN B K.	
PA	(RIEC/) RIECHMANN J L.	
PA	(CIAN/) JIANG C.	
PA	(HEAR/) HEARD J E.	
PA	(HAAR/) HAAKE V.	
PA	(CREE/) CREELMAN R A.	
PA	(RATC/) RATCLIFFE O.	
PA	(ADAM/) ADAM L J.	
PA	(REUB/) REUBER T L.	
PA	(KEDD/) KEDDIE J.	
PA	(BROU/) BROUN P E.	
PA	(PIIG/) PILGRIM M L.	
PA	(DUBE/) DUBELT A N.	
PA	(PINE/) PINEDA O.	
XX	(YUGG/) YU G.	
PI	Sherman BK, Riechmann J, Jiang C, Heard J, Haake V, Crieleman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,	

PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
 XX WPI; 2004-132245/13.  
 XX  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX  
 PS Claim 1; SEQ ID NO 802; 435bp; English.  
 XX  
 CC The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glyphosate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure; change in stem bifurcations; altered branching  
 CC pattern; reduced apical dominance; reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanin; or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor, and an orthologue of Arabidopsis thaliana  
 CC transcription factors isolated in the invention, that can be used in the  
 CC creation of a transgenic plant with altered traits.  
 CC  
 XX  
 SQ Sequence 160 AA;  
 Query Match 92.3%; Score 423.5; DB 8; Length 160;  
 Best Local Similarity 85.1%; Pred. No. 2.2e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPIANISIRIMKALPNXGKXXXXXXIAKDAKXTXQCVSEFISFITSASXKC 60  
 DB 27 REODRYLPIANISIRIMKALPNXGK-----IAKDAKXTXQCVSEFISFITSASXKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFEDYIBPLKVLXYYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFEDYIBPLKVLARYREAG 120  
 RESULT 2  
 ADS16959 standard; protein; 160 AA.  
 XX  
 AC ADS16959;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Plant polypeptide #18.  
 XX  
 KM Abiotic stress tolerance; LIL-related CCAAT transcription factor;  
 KM B domain; heat tolerance; drought stress tolerance; cold tolerance;  
 KM salt stress tolerance; MYB-related transcription factor;  
 KM seedling germination.  
 XX  
 OS Undentified.  
 XX  
 PN WO2004076638-A2.  
 XX  
 PD 10-SBP-2004.  
 XX  
 PF 25-FEB-2004; 2004WO-US005654.  
 XX  
 PR 25-FEB-2003; 2003US-00374780.  
 PR 30-SBP-2003; 2003US-00675852.  
 XX

PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Sherman BK, Riechmann JB, Ratcliffe O, Jiang C, Heard JB;  
 PI Haake V, Creelman RA, Adam LJ, Reuber LT, Keddle JS, Dubell AN;  
 PI Pineda O, Reppel P, Century KS, Guterson NI, Yu G, Brown PB;  
 PI Kumamoto RW, Pilgrim ML;  
 XX  
 DR WPI; 2004-653405/63.  
 XX  
 PT New transgenic plant having increased abiotic stress tolerance as  
 PT compared to non-transgenic plants of the same species, useful in  
 PT bioinformatic research methods.  
 XX  
 PS Disclosure; Fig 10; 297bp; English.  
 XX  
 CC The invention relates to a transgenic plant having increased abiotic  
 CC stress tolerance as compared to non-transgenic plants of the same  
 CC species, where the transgenic plant comprises in its genome a transgene  
 CC encoding a polypeptide member of the G482 subclade of the non-LBCL-like  
 CC clade of proteins of the LIL-related CCAAT transcription factor family,  
 CC where overexpression of the polypeptide member confers abiotic stress  
 CC tolerance. The invention also relates to a seed from the transgenic  
 CC plant, a method for producing a transgenic plant having increased  
 CC tolerance to abiotic stress comprising providing an expression vector  
 CC comprising the polynucleotide sequence encoding the polypeptide, and  
 CC regulatory elements operably linked to the nucleotide sequence, where the  
 CC regulatory elements are effective to control expression of the nucleotide  
 CC sequence in a target plant, introducing the expression vector into a  
 CC plant cell, growing the plant cell, allowing the plant to overexpress the  
 CC polypeptide and identifying one or more abiotic stress tolerant plants  
 CC produced by comparing the one or more abiotic stress tolerant plants with  
 CC one or more non-transgenic plants of the same species, and a method for  
 CC increasing a plant's tolerance to abiotic stress comprising providing the  
 CC vector cited above and transforming the target plant with the vector to  
 CC generate a transformed plant with increased tolerance to abiotic stress,  
 CC compared to non-transgenic plants of the same species. The transgenic  
 CC plant comprises a polypeptide comprising a B domain. The B domain binds  
 CC to DNA at a transcription-regulating region comprising the motif CCAAT,  
 CC where the binding regulates transcription of the DNA. The regulation of  
 CC transcription confers increased abiotic stress tolerance in the  
 CC transgenic plant as compared to non-transgenic plants of the same  
 CC species. The abiotic stress tolerance is selected from heat tolerance,  
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The  
 CC transgenic plant further comprises a constitutive, inducible, or tissue-  
 CC specific promoter operably linked to the recombinant polynucleotide. The  
 CC recombinant polynucleotide is incorporated into an expression vector  
 CC comprising one or more regulatory elements that are effective to control  
 CC expression of the recombinant polynucleotide in a target plant. The  
 CC transgenic plant is a cultured host cell. The transgenic plant can  
 CC comprise in its genome a transgene encoding a polypeptide member of the  
 CC MYB-related transcription factor family, where overexpression of the  
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant  
 CC is useful in bioinformatic research methods. The invention provides  
 CC transgenic plants with improved seedling germination and performance  
 CC under conditions of limited nitrogen. This sequence represents a  
 CC polypeptide used in the scope of the invention.  
 CC  
 XX  
 SQ Sequence 160 AA;  
 Query Match 92.3%; Score 423.5; DB 8; Length 160;  
 Best Local Similarity 85.1%; Pred. No. 2.2e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPIANISIRIMKALPNXGKXXXXXXIAKDAKXTXQCVSEFISFITSASXKC 60  
 DB 27 REODRYLPIANISIRIMKALPNXGK-----IAKDAKXTXQCVSEFISFITSASXKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFEDYIBPLKVLXYYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFEDYIBPLKVLARYREAG 120  
 RESULT 3



AD063706  
 ID AD063706 standard; protein: 173 AA.  
 XX  
 AC AD063706;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Transcription factor G3471 orthologous sequence, SEQ ID 2173.  
 XX  
 XX plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 KM osmotic stress tolerance; cold tolerance; heat tolerance;  
 KM low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KM glyphosate resistance; flowering; fertility; seed development.  
 XX  
 OS Glycine max.  
 XX  
 PN MO2004031349-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 18-SEP-2003; 2003MO-US030292.  
 XX  
 PR 18-SEP-2002; 2002US-0411837P.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 24-APR-2003; 2003US-0465809P.  
 XX  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 PI Jjiang C, Heard JB, Ratcliffe O, Creelman RA, Adam LJ, Reuber TJ;  
 PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK,  
 PI WPI; 2004-330163/30.  
 XX  
 DR N-PSDB; AD063705.  
 XX  
 PT New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.  
 XX  
 PS Disclosure, SEQ ID NO 2173; 510pp; English.  
 XX  
 CC The present invention relates to novel plant transcription factor  
 CC proteins (I) and nucleotide sequences (II) (AD061534-AD063778). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (II), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stresses,  
 CC increased tolerance to osmotic stress, increased tolerance to cold;  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
 CC increased tolerance to multiple fungal pathogens, increased resistance to  
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced  
 CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC avoidance, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprenyl content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and

CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 173 AA;  
 XX  
 Query Match 92.3%; Score 423.5; DB 8; Length 173;  
 Best Local Similarity 85.1%; Pred. No. 2,5e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 XX  
 QY 1 REODRYLPIANISRIKKALPXNGKXXXXXXIAKDAKTXQECVSEFISFISBA5XKC 60  
 DB 26 REODRYLPIANISRIKKALPXNGK-----IAKDAKTXQECVSEFISFISBA5XKC 78  
 QY 61 QXERKTINGDDLLMAMATLGFEDYTEPLKLYLXXYREXEG 101  
 DB 79 QXERKTINGDDLLMAMATLGFEDYTEPLKLYLARBREAEG 119  
 XX  
 RESULT 4  
 AD0616957  
 ID AD0616957 standard; protein: 173 AA.  
 XX  
 AC AD0616957;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Plant polypeptide #16.  
 XX  
 KM Abiotic stress tolerance; LIL-related CCAT transcription factor;  
 KM B domain; heat tolerance; drought stress tolerance; cold tolerance;  
 KM salt stress tolerance; MYB-related transcription factor;  
 KM seedling germination.  
 XX  
 OS Undentified.  
 XX  
 PN WO2004076638-A2.  
 XX  
 PD 10-SEP-2004.  
 XX  
 PF 25-FEB-2004; 2004MO-US005654.  
 XX  
 PR 25-FEB-2003; 2003US-00374780.  
 PR 30-SEP-2003; 2003US-00675852.  
 XX  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 PI Sherman BK, Riechmann JL, Ratcliffe O, Jjiang C, Heard JB;  
 PI Haake V, Creelman RA, Adam LJ, Reuber TJ, Keddie JS, Dubell AN;  
 PI Plameda O, Repetti PP, Century KS, Guttersen NI, Yu G, Brown PB;  
 PI Kumimoto RW, Pilgrim ML;  
 XX  
 DR WPI; 2004-653405/63.  
 XX  
 PT New transgenic plant having increased abiotic stress tolerance as  
 PT compared to non-transgenic plants of the same species, useful in  
 PT bioinformatic research methods.  
 XX  
 PS Disclosure; Fig 10; 297p; English.  
 XX  
 CC The invention relates to a transgenic plant having increased abiotic  
 CC stress tolerance as compared to non-transgenic plants of the same  
 CC species, where the transgenic plant comprises in its genome a transgene  
 CC encoding a polypeptide member of the G482 subclade of the non-LBEC1-like  
 CC clade of proteins of the LIL-related CCAT transcription factor family,  
 CC where overexpression of the polypeptide member confers abiotic stress  
 CC tolerance. The invention also relates to a seed from the transgenic  
 CC plant, a method for producing a transgenic plant having increased  
 CC tolerance to abiotic stress comprising providing an expression vector  
 CC comprising the polynucleotide sequence encoding the polypeptide, and  
 CC regulatory elements operably linked to the nucleotide sequence, where the  
 CC regulatory elements are effective to control expression of the nucleotide

CC sequence in a target plant, introducing the expression vector into a  
 CC plant cell, growing the plant cell, allowing the plant to overexpress the  
 CC polypeptide and identifying one or more abiotic stress tolerant plants so  
 CC produced by comparing the one or more abiotic stress tolerant plants with  
 CC one or more non-transgenic plants of the same species, and a method for  
 CC increasing a plant's tolerance to abiotic stress comprising providing the  
 CC vector cited above and transforming the target plant with the vector to  
 CC generate a transformed plant with increased tolerance to abiotic stress,  
 CC compared to non-transgenic plants of the same species. The transgenic  
 CC plant comprises a polypeptide comprising a B domain. The B domain binds  
 CC to DNA at a transcription-regulating region comprising the motif CCAAT,  
 CC where the binding regulates transcription of the DNA. The regulation of  
 CC transcription confers increased abiotic stress tolerance in the  
 CC transgenic plant as compared to non-transgenic plants of the same  
 CC species. The abiotic stress tolerance is selected from heat tolerance,  
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The  
 CC transgenic plant further comprises a constitutive, inducible, or tissue-  
 CC specific promoter operably linked to the recombinant polynucleotide. The  
 CC recombinant polynucleotide is incorporated into an expression vector  
 CC comprising one or more regulatory elements that are effective to control  
 CC expression of the recombinant polynucleotide in a target plant. The  
 CC transgenic plant is a cultured host cell. The transgenic plant can  
 CC comprise in its genome a transgene encoding a polypeptide member of the  
 CC MYB-related transcription factor family, where overexpression of the  
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant  
 CC is useful in bioinformatic research methods. The invention provides  
 CC transgenic plants with improved seedling germination and performance  
 CC under conditions of limited nitrogen. This sequence represents a  
 CC polypeptide used in the scope of the invention.

CC Sequence 173 AA;

CC Query Match 92.3%; Score 423.5; DB 8; Length 173;  
 CC Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 CC Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

CC QY 1 REODRYLPIANISRIKKALPXNGKXXXXXXIAKDAKXTXOCVSEFISFITSASXKC 60  
 CC DB 26 REODRYLPIANISRIKKALPPNGK-----IAKADKDTMOCVSEFISFITSASXKC 78  
 CC QY 61 QXERKRTINGDDLLMAMATGFFEDYIEPLKVTLYXXYREXEG 101  
 CC DB 79 QXERKRTINGDDLLMAMATGFFEDYIEPLKVTLYARREXEG 119

CC RESULT 5

CC ID ADO63718 standard; protein; 174 AA.

CC AC ADO63718;

CC DT 15-JUL-2004 (first entry)

CC XX Transcription factor G3477 orthologous sequence, SEQ ID 2185.

CC XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;

CC KM osmotic stress tolerance; cold tolerance; heat tolerance;

CC KM low nitrogen tolerance; low phosphate tolerance; fungal disease;

CC KM glycosylase resistance; flowering; fertility; seed development.

CC OS glycine max.

CC XX WO2004031349-A2.

CC PN 15-APR-2004.

CC XX 18-SEP-2003; 2003WO-US030292.

CC XX 18-SEP-2002; 2002US-0411837P.

CC PR 17-DEC-2002; 2002US-0434166P.

CC PR 24-APR-2003; 2003US-0465809P.

CC PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX Jiang C, Heard JE, Ratcliffe O, Creelman JS, Adam LJ, Reuber TL,  
 PI Riechmann JL, Haake V, Dubell AN, Keddie SA, Sherman BK,  
 DR WPI; 2004-330163/30.  
 XX N-PSDB; ADO63717.

PT New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.

PS Disclosure; SEQ ID NO 2185; 510pp; English.

XX The present invention relates to novel plant transcription factor  
 CC proteins (i) and nucleotide sequences (ii) (ADO61534-ADO63718). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (ii), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stress,  
 CC increased tolerance to osmotic stress, increased tolerance to cold,  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
 CC increased tolerance to multiplicity fungal pathogens, increased resistance to  
 CC glycosylase, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced  
 CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC avoidance, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprotein content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
 CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC CC ftp.wipo.int/pub/published\_pct\_sequences.

CC SQ Sequence 174 AA;

CC Query Match 92.3%; Score 423.5; DB 8; Length 174;  
 CC Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 CC Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

CC QY 1 REODRYLPIANISRIKKALPXNGKXXXXXXIAKDAKXTXOCVSEFISFITSASXKC 60  
 CC DB 27 REODRYLPIANISRIKKALPPNGK-----IAKADKDTMOCVSEFISFITSASXKC 79  
 CC QY 61 QXERKRTINGDDLLMAMATGFFEDYIEPLKVTLYXXYREXEG 101  
 CC DB 80 QXERKRTINGDDLLMAMATGFFEDYIEPLKVTLYARREXEG 120

CC RESULT 6

CC ID ADO63704 standard; protein; 174 AA.

CC AC ADO63704;

CC DT 15-JUL-2004 (first entry)

Transcription factor G3470 orthologous sequence, SEQ ID 2171.

Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.

Glycine max.

WO2004031349-A2.

15-APR-2004.

18-SEP-2003; 2003WO-US030292.

18-SEP-2002; 2002US-0411837P.

17-DEC-2002; 2002US-0434166P.

24-APR-2003; 2003US-0465809P.

(MEND-) MENDEL BIOTECHNOLOGY INC.

Jiang C, Heard JB, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL, Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK, WPI, 2004-330163/30.

N-PSDB; ADO63703.

New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.

Disclosure; SEQ ID NO 2171; 510pp; English.

The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, including fungal disease and particularly Erysiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, altered trichome structure, altered root development, altered shade avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased seed wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedpremyl content, altered leaf premyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 174 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 174;  
Beet Local Similarity 85.1%; Pred. No. 2.5e-54;  
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1

Qy 1 REODRYLPLANTSRIMKALPYNGKXXXXXXXXXIAADAKTKXOCVSEFISFISEASXKC 60  
Db 27 RRODHYLPLANTSRIMKALPPNGK-----IADAKTKMCEVSEFISFISEASEK 79  
Qy 61 QXKRTKINGDDLWAMATLGFEDYIEPLKVIYIXYREXEG 101  
Db 80 QXKRTKINGDDLWAMATLGFEDYIEPLKVIYIARYREAEG 120

RESULT 7  
ID ADL16958 standard; protein; 174 AA.  
XX ADL16958;  
AC ADL16958;  
DT 02-DEC-2004 (first entry)  
XX  
DE Plant polypeptide #17.  
XX  
KW Abiotic stress tolerance; LIL-related CCAAT transcription factor;  
KW B domain; heat tolerance; drought stress tolerance; cold tolerance;  
KW salt stress tolerance; MYB-related transcription factor;  
KW seedling germination.  
XX  
OS Unidentified.  
XX  
XX WO2004076638-A2.  
PM 10-SEP-2004.  
PD 10-SEP-2004.  
XX  
PF 25-FEB-2004; 2004MO-US005654.  
XX  
PR 25-FEB-2003; 2003US-00374780.  
PR 30-SEP-2003; 2003US-00675852.  
XX  
XX  
XX (MENDL) MENDEL BIOTECHNOLOGY INC.  
PA  
XX  
XX Sherman BK, Riechmann JL, Ratcliffe O, Jiang C, Heard JB;  
PI Haake V, Creelman RA, Adam LJ, Reuber LT, Keddie JS, Dubell AN;  
PI Pineda O, Repetti PP, Century KS, Guterson NI, Yu G, Brown PS;  
PI Kumamoto RW, Pilgrim ML;  
XX  
XX WPI; 2004-653405/63.  
XX  
XX  
XX New transgenic plant having increased abiotic stress tolerance as  
PT compared to non-transgenic plants of the same species, useful in  
PT biotransformatic research methods.  
XX  
XX  
XX Disclosure; Fig 10; 297pp; English.

XX  
XX The invention relates to a transgenic plant having increased abiotic  
CC stress tolerance as compared to non-transgenic plants of the same  
CC species, where the transgenic plant comprises in its genome a transgene  
CC encoding a polypeptide member of the G482 subclade of the non-LRC1-like  
CC clade of proteins of the LIL-related CCAAT transcription factor family,  
CC where overexpression of the polypeptide member confers abiotic stress  
CC tolerance. The invention also relates to a seed from the transgenic  
CC plant, a method for producing a transgenic plant having increased  
CC tolerance to abiotic stress comprising providing an expression vector  
CC comprising the polynucleotide sequence encoding the polypeptide, and  
CC regulatory elements operably linked to the nucleotide sequence, where the  
CC regulatory elements are effective to control expression of the nucleotide  
CC sequence in a target plant, introducing the expression vector into a  
CC plant cell, growing the plant cell, allowing the plant to overexpress the  
CC polypeptide and identifying one or more abiotic stress tolerant plants so  
CC produced by comparing the one or more abiotic stress tolerant plants with  
CC one or more non-transgenic plants of the same species, and a method for  
CC increasing a plant's tolerance to abiotic stress comprising providing the

CC vector cited above and transforming the target plant with the vector to  
 CC generate a transformed plant with increased tolerance to abiotic stress.  
 CC plant comprises a non-transgenic plant of the same species. The transgenic  
 CC plant comprises a polypeptide comprising a B domain. The B domain binds  
 CC to DNA at a transcription-regulating region comprising the motif CCAT, where  
 CC the binding regulates transcription of the DNA. The regulation of  
 CC transcription confers increased abiotic stress tolerance in the  
 CC transgenic plant as compared to non-transgenic plants of the same  
 CC species. The abiotic stress tolerance is selected from heat tolerance,  
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The  
 CC transgenic plant further comprises a constitutive, inducible, or tissue-  
 CC specific promoter operably linked to the recombinant polynucleotide. The  
 CC recombinant polynucleotide is incorporated into an expression vector  
 CC comprising one or more regulatory elements that are effective to control  
 CC expression of the recombinant polynucleotide in a target plant. The  
 CC transgenic plant is a cultured host cell. The transgenic plant can  
 CC comprise in its genome a transgene encoding a polypeptide member of the  
 CC MYB-related transcription factor family, where overexpression of the  
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant  
 CC is useful in bioinformatic research methods. The invention provides  
 CC transgenic plants with improved seedling germination and performance  
 CC under conditions of limited nitrogen. This sequence represents a  
 CC polypeptide used in the scope of the invention.

CC Sequence 174 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPANISRIKMKALPXNGKXXXXXXIAKDAKXTXORCVSEFISFITSASXKC 60  
 Db 27 REODRYLPANISRIKMKALPXNGK-----IAKDAKXTXORCVSEFISFITSASEKC 79  
 QY 61 QXERKRTINGDDLLMAMATGFEFDYIEPLKVTLYXXYREXEG 101  
 Db 80 QXERKRTINGDDLLMAMATGFEFDYIEPLKVTLYXXYREXEG 120

RESULT 8

ABG70264  
 ID ABG70264 standard; protein; 178 AA.

AC ABG70264;

XX 21-OCT-2002 (first entry)

DE IEC-1-related transcription factor polypeptide #17.

XX Maize; balsam pear; eucalyptus; rice; soybean; bread wheat; plant;

KM leafy cotyledon1-related transcription factor; plant embryogenesis;

KM LEC1-related transcription factor; thale cress; plant breeding.

OS Zea mays.

XX WO200257439-A2.

XX 25-JUL-2002.

XX 24-OCT-2001; 2001MO-US050908.

XX 24-OCT-2000; 2000US-0242739P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Cahoon RE, Klein TM;

XX WPI; 2002-590737/63.

PT New isolated polynucleotide encoding leafy cotyledon1-related  
 PT transcription factor, useful in facilitating studies for better  
 PT understanding of plant embryogenesis, or providing genetic tools for the  
 PT manipulation of plant growth.

XX Example 3; Fig 1; 63pp; English.

XX The invention relates to a polypeptide with leafy cotyledon1 (LEC1) -  
 CC related transcription factor activity and its associated polynucleotide.  
 CC The sequences are useful in facilitating studies for better understanding  
 CC of plant embryogenesis, and providing genetic tools for the manipulation  
 CC of plant growth. All or a substantial portion of the polynucleotides are  
 CC useful as probes for genetically and physically mapping the genes that  
 CC they are a part of, and as markers for traits linked to the genes, which  
 CC are useful in plant breeding to develop lines with desired phenotypes.  
 CC The probes may also be used in direct fluorescence in situ hybridisation  
 CC mapping. Sequences ABG70248-ABG70267 represent LEC1-related transcription  
 CC factor polypeptides of the invention

XX Sequence 178 AA;

Query Match 91.0%; Score 417.5; DB 5; Length 178;  
 Best Local Similarity 83.2%; Pred. No. 2e-53;  
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPANISRIKMKALPXNGKXXXXXXIAKDAKXTXORCVSEFISFITSASXKC 60  
 Db 30 REODRYLPANISRIKMKALPXNGK-----IAKDAKXTXORCVSEFISFITSASDKC 82  
 QY 61 QXERKRTINGDDLLMAMATGFEFDYIEPLKVTLYXXYREXEG 101  
 Db 83 QXERKRTINGDDLLMAMATGFEFDYIEPLKVTLYXXYREXEG 123

RESULT 9  
 ABR40821  
 ID ABR40821 standard; protein; 178 AA.

AC ABR40821;

XX 16-MAY-2003 (first entry)

DE Zea mays oil trait related protein sequence SEQ ID NO:413.

XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;

KM receptor-like protein kinase; mitogen activated protein kinase; oil;

KM LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;

KM CKC-like transcription factor; antisense inhibition; co-suppression;

XX transgenic plant.

XX Zea mays.

XX WO2003002751-A2.

XX 09-JAN-2003.

XX 27-JUN-2002; 2002MO-US020152.

XX 29-JUN-2001; 2001US-0301913P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Farnold OO, Harvell LT,

XX Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,

XX Tarczynski MC;

XX WPI; 2003-201509/19.

PT Novel nucleotide fragment encoding polypeptides having receptor-like  
 PT protein kinase activity, caleosin-like activity, useful for altering oil  
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.  
 PS Claim 12; Page 451; 542pp; English.  
 CC The present invention describes an isolated nucleotide fragment (1)  
 CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a

CC polypeptide (pp) having receptor-like protein kinase activity, mitogen  
 CC activated protein (MAP)-kinase activity, LIPIS-like transcription factor  
 CC activity, calcein-like activity, ATP citrate lyase activity, SNF1-like  
 CC activity, calcein-like transcription factor activity. Also described: (1)  
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or  
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV) or  
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)  
 CC obtained from (V). (I) or its part can be used in antisense  
 CC inhibition or co-suppression in a transformed plant. (III) is useful for  
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,  
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for  
 CC creating transgenic plants having altered lipid profiles. (I) can also be  
 CC used as a hybridisation probe. ACC00626 to ACC00686 and ABR40591 to  
 CC ABR40879 represent sequences used in the exemplification of the present  
 CC invention  
 CC  
 XX  
 SQ Sequence 178 AA;  
 Query Match 91.0%; Score 417.5; DB 6; Length 178;  
 Best Local Similarity 83.2%; Pred. No. 2e-53; Mismatches 8; Indels 7; Gaps 1;  
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFISEASXKC 60  
 DB 30 REODRFLPINISIRIMKKAIPANGK-----IAKDAKXTXQECVSEFISFISEASDKC 82  
 QY 61 QXERKRTINGDDLLMAMATGFPEDYIEPLKVIYLLXXREXEG 101  
 DB 83 QREKRTINGDDLLMAMATGFPEDYIEPLKVIYLLXXREXEG 123  
 RESULT 10  
 ADI42322  
 ID ADI42322 standard; protein; 178 AA.  
 XX  
 AC ADI42322;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Plant transcription factor #302.  
 XX  
 KW transgenic; plant; enhanced tolerance to abiotic stresses;  
 KW glycosphate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor; gene; ds.  
 XX  
 OS Zea mays.  
 XX  
 PN US2004019927-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 25-FEB-2003; 2003US-00374780.  
 XX  
 PR 18-APR-2001; 2001US-00837944.  
 XX  
 PA (SHER/) SHERMAN B. K.  
 PA (RIEC/) RIECHMANN J. L.  
 PA (JIAN/) JIANG C.  
 PA (HEAR/) HEARD J. B.  
 PA (HAAK/) HAAKE V.  
 PA (CREE/) CREELMAN R. A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L. J.  
 PA (REUB/) REUBER T. L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P. E.  
 PA (PILG/) PILGRIM M. L.

PA (DUBE/) DUBBEL A. N.  
 PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.  
 XX  
 PI Sherman BK, Riechmann JL, Jiang C, Heard JB, Haake V,  
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,  
 PI Pilgrim ML, Dubbel AN, Pineda O, Yu G,  
 XX  
 DR WPI; 2004-132245/13.  
 XX  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX  
 PS Claim 1; SEQ ID NO 785; 435bp; English.  
 XX  
 CC The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produced a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glycosphate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure, change in stem bifurcations, altered branching  
 CC pattern, reduced apical dominance, reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor, and an orthologue of Arabidopsis thaliana  
 CC transcription factors isolated in the invention, that can be used in the  
 CC creation of a transgenic plant with altered traits.  
 XX  
 SQ Sequence 178 AA;  
 Query Match 91.0%; Score 417.5; DB 8; Length 178;  
 Best Local Similarity 83.2%; Pred. No. 2e-53; Mismatches 8; Indels 7; Gaps 1;  
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFISEASXKC 60  
 DB 30 REODRFLPINISIRIMKKAIPANGK-----IAKDAKXTXQECVSEFISFISEASDKC 82  
 QY 61 QXERKRTINGDDLLMAMATGFPEDYIEPLKVIYLLXXREXEG 101  
 DB 83 QREKRTINGDDLLMAMATGFPEDYIEPLKVIYLLXXREXEG 123  
 RESULT 11  
 ADI42323  
 ID ADI42323 standard; protein; 179 AA.  
 XX  
 AC ADI42323;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Plant transcription factor #303.  
 XX  
 KW transgenic; plant; enhanced tolerance to abiotic stresses;  
 KW glycosphate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor; gene; ds.

OS Zea mays.

XX US2004019927-A1.

XX 29-JAN-2004.

XX 25-FEB-2003; 2003US-00374780.

XX 18-APR-2001; 2001US-00637944.

XX (SHER/) SHERMAN B. K.

XX (RIEC/) RIECHMANN J. L.

XX (JIANG/) JIANG C.

XX (HEAR/) HEARD J. B.

XX (HAAR/) HAARE V.

XX (CREE/) CREEHMAN R. A.

XX (RATC/) RATCLIFFE O.

XX (ADAM/) ADAM L. J.

XX (REUB/) REUBER T. L.

XX (KEDD/) KEDDIE J.

XX (BROU/) BROUN P. E.

XX (PIILG/) PILGRIM M. L.

XX (DUEB/) DUEBEL A. N.

XX (PINE/) PINEDA O.

XX (YUGG/) YU G.

XX Sherman BK, Riechmann JL, Jiang C, Heard JB, Haake V;

XX Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE;

XX Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX WPI; 2004-132245/13.

XX New transgenic plant comprising a recombinant polynucleotide of any one

XX PT of more than 500 nucleotide sequences, useful in bioinformatic search

XX PT methods.

XX Claim 1; SEQ ID NO 786; 435bp; English.

XX The invention describes a transgenic plant comprising a recombinant

XX CC polynucleotide of any one of more than 500 nucleotide sequences fully

XX CC defined in the specification or its complement. The method of the

XX CC invention can be used to produce a plant having altered traits such as:

XX CC enhanced tolerance to abiotic stress; glyphosate tolerance; hormone

XX CC sensitivity; disease resistance; sugar sensing; early or late flowering;

XX CC altered flower structure, change in stem bifurcations, altered branching

XX CC pattern, reduced apical dominance, reduced trichome density; lack of

XX CC trichomes; reduced ectopic trichome development; altered trichome

XX CC development; increase in trichome number; altered stem morphology;

XX CC increased root growth; increased root hairs; altered seed development;

XX CC altered cell proliferation or cell differentiation; rapid development;

XX CC premature senescence; increased necrosis; increase in seedling or plant

XX CC size; decreased plant size; leaf morphology; seed morphology; seed

XX CC biochemistry; increase in root anthocyanins; increase in plant

XX CC anthocyanins; or alteration in light response or shade avoidance. The

XX CC transgenic plant, polynucleotides and polypeptides are useful in

XX CC bioinformatic search methods. This is the amino acid sequence of a plant

XX CC transcription factor, and an orthologue of Arabidopsis thaliana

XX CC transcription factors isolated in the invention, that can be used in the

XX CC creation of a transgenic plant with altered traits.

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RESULT 12

ADCC23665

ID ADCC23665 standard; protein; 290 AA.

XX AC ADCC23665;

XX 18-DEC-2003 (first entry)

XX Polypeptide involved in altering plant oil phenotype (seqid 170).

XX oil phenotype; plant; breeding; Hap transcription factor;

XX lipid biosynthesis; Hap2-like; Hap5-like; Hap3/lec1-like; soybean.

XX glycine max.

XX WO2003001902-A2.

XX 09-JAN-2003.

XX 27-JUN-2002; 2002WO-US022086.

XX 29-JUN-2001; 2001US-0301913P.

XX (DUPO ) DU PONT DE NEMOURS &amp; CO B. I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Allen WB, Cahoon RE, Farnold OO, Harwell LT, Helentjaris TG, Li C;

XX Lowe KS, Oliveira IC, Shen B, Tarczy-Hart MC;

XX WPI; 2003-210187/20.

XX N-PSDB; ADCC23664.

XX Novel nucleotide fragment encoding polypeptides having Hap2, Hap5 or

XX PT Hap3/lec1 like activity useful for altering oil phenotypes in plants such

XX PT as sunflower, coconut, soybean, wheat and rice.

XX Claim 11; SEQ ID NO 170; 202bp; English.

XX The present invention relates to a novel method for altering oil

XX CC phenotype in plants through the controlled expression of selective genes,

XX CC useful in plant breeding. Specifically, it refers to the isolated nucleic

XX CC acid sequences of cDNA clones that encode polypeptides homologous to

XX CC proteins of the Hap transcription factor family. Hap proteins have been

XX CC shown to be regulators of several important genes involved in lipid

XX CC biosynthesis, such as fatty acid synthase, and are also involved in

XX CC diverse processes from cell cycle regulation to metabolic control and

XX CC homeostasis. The present invention describes proteins having Hap2-like or

XX CC Hap5-like transcription factor activity, or alternatively Hap3/lec1-like

XX CC activity, which can be used to transform plants such that it is possible

XX CC to select those with an altered phenotype. This polypeptide sequence is a

XX CC protein homologous to those involved in altering plant oil phenotypes, in

XX CC an exemplification of the invention.

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RESULT 13

AAG04651

ID AAG04651 standard; protein; 141 AA.

XX AC AAG04651;

XX 18-DEC-2003 (first entry)

XX Polypeptide involved in altering plant oil phenotype (seqid 170).

XX oil phenotype; plant; breeding; Hap transcription factor;

XX lipid biosynthesis; Hap2-like; Hap5-like; Hap3/lec1-like; soybean.

XX glycine max.

XX WO2003001902-A2.

XX 09-JAN-2003.

XX 27-JUN-2002; 2002WO-US022086.

XX 29-JUN-2001; 2001US-0301913P.

XX (DUPO ) DU PONT DE NEMOURS &amp; CO B. I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Allen WB, Cahoon RE, Farnold OO, Harwell LT, Helentjaris TG, Li C;

XX Lowe KS, Oliveira IC, Shen B, Tarczy-Hart MC;

XX WPI; 2003-210187/20.

XX N-PSDB; AAG04651.

XX Novel nucleotide fragment encoding polypeptides having Hap2, Hap5 or

XX PT Hap3/lec1 like activity useful for altering oil phenotypes in plants such

XX PT as sunflower, coconut, soybean, wheat and rice.

XX Claim 11; SEQ ID NO 170; 202bp; English.

XX The present invention relates to a novel method for altering oil

XX CC phenotype in plants through the controlled expression of selective genes,

XX CC useful in plant breeding. Specifically, it refers to the isolated nucleic

XX CC acid sequences of cDNA clones that encode polypeptides homologous to

XX CC proteins of the Hap transcription factor family. Hap proteins have been

XX CC shown to be regulators of several important genes involved in lipid

XX CC biosynthesis, such as fatty acid synthase, and are also involved in

XX CC diverse processes from cell cycle regulation to metabolic control and

XX CC homeostasis. The present invention describes proteins having Hap2-like or

XX CC Hap5-like transcription factor activity, or alternatively Hap3/lec1-like

XX CC activity, which can be used to transform plants such that it is possible

XX CC to select those with an altered phenotype. This polypeptide sequence is a

XX CC protein homologous to those involved in altering plant oil phenotypes, in

XX CC an exemplification of the invention.

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XX  
AC AAG04651;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 757.  
XX  
KM Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridization assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132407P.  
PR 05-MAY-1999; 99US-0132484P.  
PR 06-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
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PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
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PR 18-JUN-1999; 99US-0139461P.  
  
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PR 19-JUL-1999; 99US-0144325P.  
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PR 19-JUL-1999; 99US-0144332P.  
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PR 25-AUG-1999; 99US-0150566P.  
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PR 05-OCT-1999; 99US-0157753P.  
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PR 22-OCT-1999; 99US-0160961P.  
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PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 90.3%; Score 414.5; DB 3; Length 141;  
Best Local Similarity 81.2%; Pred. No. 4.1e-53;  
Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXAKDAKXTXQCVSEFFISFITSASXKC 60  
DB 20 REODRYLPINISIRIMKALPPNKG-----IGKDAKDTVOECVSEFFISFITSASDKC 72  
QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVLVXXYREXEG 101  
DB 73 QXERKRTVNGDDLLMAMATLGFEDYIEPLKYLARIYRELEG 113

RESULT 14  
ADE37175  
ID ADE37175 standard; protein; 141 AA.  
AC ADE37175;  
XX

DT 29-JAN-2004 (first entry)  
XX  
DE Plant yield related protein from clone G481.  
XX  
XX transcription factor; tolerance; environmental condition;  
XX microbial disease; fungal disease; viral disease; pest infestation;  
XX herbicide sensitivity; heavy metal tolerance; heavy metal uptake;  
XX growth improvement; photocondition; nutrient uptake; hormone sensitivity;  
XX transgenic plant.  
XX  
OS Arabidopsis thaliana.  
XX  
XX  
PN MO2003014327-A2.  
XX  
XX  
PD 20-FEB-2003.  
XX  
XX  
PF 09-AUG-2002; 2002MO-US026966.  
XX  
XX  
PR 09-AUG-2001; 2001US-0310847P.  
PR 19-NOV-2001; 2001US-0336049P.  
PR 11-DEC-2001; 2001US-0338692P.  
PR 14-UTN-2002; 2002US-00171468.  
XX  
XX  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
XX  
XX Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LD, Dubell AN;  
PI Rattcliffe O, Pineda O, Yu GL, Brown PE,  
DR N-PSDB; ADE37174.  
XX  
XX WPI; 2003-256576/25.  
XX  
XX  
PT New stress-related transcription factor polynucleotides and polypeptides,  
PT useful for producing transgenic plants with e.g. improved tolerance to  
PT diseases or pests, decreased herbicide sensitivity, or improved nutrient  
PT uptake.  
XX  
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PS Disclosure; SEQ ID NO 114; 470bp; English.  
XX  
XX  
CC The invention relates to a number of cDNA sequence and their encoded  
CC proteins which are especially transcription factor cDNAs and their  
CC proteins. The isolated or recombinant polynucleotide is useful for  
CC producing a modified plant with a modified trait, e.g. enhanced tolerance  
CC to environmental conditions, improved tolerance to microbial, fungal or  
CC viral diseases, improved tolerance to pest infestation, decreased  
CC herbicide sensitivity, improved tolerance of heavy metals, or enhanced  
CC ability to take up heavy metals, improved growth under poor  
CC photoconditions, improved nutrient uptake, or reduced hormone  
CC sensitivity. The transgenic plants are useful for growing a progeny plant  
CC comprising the desired trait. The polynucleotides and polypeptides are  
CC also useful in bioinformatic search methods. This sequence represents one  
CC of the proteins of the invention.  
XX  
XX  
SQ Sequence 141 AA;

Query Match 90.3%; Score 414.5; DB 7; Length 141;  
Best Local Similarity 81.2%; Pred. No. 4.1e-53;  
Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXAKDAKXTXQCVSEFFISFITSASXKC 60  
DB 20 REODRYLPINISIRIMKALPPNKG-----IGKDAKDTVOECVSEFFISFITSASDKC 72  
QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVLVXXYREXEG 101  
DB 73 QXERKRTVNGDDLLMAMATLGFEDYIEPLKYLARIYRELEG 113

RESULT 15  
ADF50740  
ID ADF50740 standard; protein; 141 AA.  
AC ADF50740;  
XX



DT	12-FEB-2004 (first entry)	
XX		
DE	Thale cress transcription factor G481 protein.	
XX		
KW	thale cress; transgenic; transcription factor; G481; abiotic;	
KW	biotic stress; drought; secondary metabolite; storage nutrient; sterol;	
XX	starch; leaf; flower senescence.	
OS	Arabidopsis thaliana.	
XX		
PN	US2003188330-A1.	
XX		
PD	02-OCT-2003.	
XX		
PF	18-MAR-2002; 2002US-00112887.	
XX		
PR	18-MAR-2002; 2002US-00112887.	
XX		
PA	(HEAR/) HEARD J.	
XX		
PI	Heard J;	
XX		
XX	WPI; 2003-811784/76.	
DR	N-PSDB; ADF50739.	
XX		
PT	Transgenic plants with altered traits; e.g. resistance to stress or	
PT	increased oil content, contain recombinant DNA encoding specific	
XX	transcription factors.	
XX		
PS	Claim 4; SEQ ID NO 2; 39pp; English.	
XX		
CC	This invention relates to novel genes for phenotypically modifying a	
CC	plant using transgenics. Specifically, it comprises a recombinant	
CC	polynucleotide encoding a transcription factor having an altered trait	
CC	compared with the wild-type plant and hence exhibiting an altered	
CC	phenotype or expressing an altered level of at least one gene associated	
CC	with a plant trait. The present invention describes two novel	
CC	transcription factors, identified as G481 and G486 from Arabidopsis	
CC	thaliana that provide altered phenotypic traits when over-expressed in	
CC	the seed of transgenic plants. A wide range of traits can be modified	
CC	using these transcription factors and related antisense molecules to	
CC	alter the plant's properties including tolerance of abiotic or biotic	
CC	stresses e.g. from drought or viral infection, production of secondary	
CC	metabolites and storage nutrients e.g. starch, vitamins or sterols; and	
CC	also the physical characteristics and growth can be altered to change for	
CC	example leaf and flower senescence. This polypeptide sequence is the	
CC	Arabidopsis thaliana G481 protein of the invention.	
CC		
SO	Sequence 141 AA;	
Query Match	90.3%; Score 414.5; DB 7; Length 141;	
Best Local Similarity	81.2%; Pred. No. 4,1e-53;	
Matches	82; Conservative 3; Mismatches 9; Indels 7; Gaps 1	
OY	1 REODRYLPIANISRIKCALPYNGKXXXXXXIADAKTYOECVSEFITSASKCC 60	
DB	20 REODRYLPIANISRIKCALPYNGK-----IGDADDTVOECVSEFITSASDKC 72	
OY	61 QXERKRTINGDDLLAMATLGEDEYIEPLKAYLXXYREXG 101	
DB	73 QXERKRTIVNGDDLLAMATLGEDEYIEPLKAYLARYREXG 113	

Search completed: November 17, 2005, 08:58:53  
Job time : 166 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 17, 2005, 08:43:04 ; Search time 168 Seconds  
(without alignments)  
307,857 Million cell updates/sec

Title: US-10-678-588A-8  
Perfect score: 459  
Sequence: 1 REDDRLPLANIRIMKAL.....FEDYIEPLKYLXXYREXEG 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	417.5	91.0	167	2	Q84NFO oryza sativ
2	417.5	91.0	179	1	Q84NFO zea mays (m
3	414.5	90.3	141	2	Q9SLG0 arabidopsis
4	407.5	88.8	176	2	Q67XJ2 arabidopsis
5	407.5	88.8	228	2	Q9LFF3 arabidopsis
6	402.5	87.7	173	2	Q8VYK4 arabidopsis
7	400.5	87.3	161	2	Q23310 arabidopsis
8	395.5	86.2	167	2	Q23634 arabidopsis
9	395.5	86.2	190	2	Q9FGJ3 arabidopsis
10	393.5	85.7	178	2	Q9ZQ03 arabidopsis
11	388.5	84.6	152	2	Q84VW3 arabidopsis
12	388.5	84.6	178	2	Q84NFI oryza sativ
13	388.5	84.6	189	2	Q84NFI oryza sativ
14	388.5	84.6	224	2	Q84NFI oryza sativ
15	386.5	84.2	219	2	Q6YNK1 oryza sativ
16	386.5	84.2	219	2	Q751Z7 oryza sativ
17	376.5	82.0	143	2	Q84NFI oryza sativ
18	376.5	82.0	215	2	Q84NFI oryza sativ
19	366.5	79.8	241	2	Q65XK1 oryza sativ
20	366.5	79.8	280	2	Q6YNK0 oryza sativ
21	338.5	73.7	78	2	Q84K78 goosepium b
22	338.5	73.7	204	2	Q96WFO trichoderma
23	337.5	73.5	148	2	Q630J1 rat mus
24	337.5	73.5	151	1	CBFA_CHICK
25	337.5	73.5	169	2	Q9D056 mus musculu
26	337.5	73.5	202	2	Q6WU9 mus musculu
27	337.5	73.5	206	2	Q6T2F0 mus musculu
28	337.5	73.5	207	1	CBFA_HUMAN
29	337.5	73.5	207	1	CBFA_MOUSE
30	337.5	73.5	207	1	CBFA_RAT
31	337.5	73.5	207	2	Q6RG77 equus cabal

32	337.5	73.5	224	2	Q8C590 mus musculu
33	336.5	73.3	166	2	Q00735 emericella
34	336.5	73.3	206	2	Q6DD00 xenopus lae
35	336.5	73.3	209	1	CBFA_PETMA
36	336.5	73.3	215	2	Q59848 aspergillus
37	336.5	73.3	218	2	Q86ZV5 aspergillus
38	332.5	72.4	138	2	Q7PN95 anopheles g
39	332.5	72.4	242	2	Q76256 schistosoma
40	331.5	72.2	177	2	Q942Y5 oryza sativ
41	330.5	72.0	206	2	Q73744 xenopus lae
42	330.5	70.9	160	2	Q82248 arabidopsis
43	325.5	70.9	197	2	Q8WQ01 strongyloce
44	324.5	70.7	194	2	Q6C1E2 yarrowia li
45	320.5	69.8	254	2	Q6YNJ7 oryza sativ

## ALIGNMENTS

RESULT 1	ID	Q84NFO	PRELIMINARY;	PRT;	167 AA.
AC	Q84NFO				
DT	01-JUN-2003	(TREMBLrel. 24, Created)			
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)			
DE	HAP3 (Fragment).				
GN	Name=Q84NFB;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Eriactoidae; Oryzae; Oryza.				
OX	NCBI_TaxID=39947;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=2983257; PubMed=14617083;				
RA	Myoshi K., Ito Y., Serizawa A., Kurata N.;				
RT	"OSHAP3 genes regulate chloroplast biogenesis in rice."				
RL	Plant J. 36:532-540(2003).				
DR	EMBL; AB095439; BAC76332.1; -.				
DR	HSSP; P25208; INIJ.				
DR	Gramene; Q84NFO; -.				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003677; F:DNA binding; IEA.				
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.				
DR	InterPro; IPR003956; CBFA_NFYB.				
DR	InterPro; IPR003958; CBFA_NFYB domain.				
DR	InterPro; IPR003957; CBFA_NFYB_topic.				
DR	InterPro; IPR009072; Histone-fold.				
DR	InterPro; IPR007124; Hist_TAF.				
DR	Pfam; PF00808; CBP_NFYB_HMF.1.				
DR	PRINTS; PR00615; COATSUBUNITA.				
DR	PROSITE; PS00685; CBFA_NFYB.1.				
FT	NON TER				
SQ	SEQUENCE 167 AA; 17971 MW; FB85544A22CE0495 CRC64;				
Query Match		91.0%; Score 417.5; DB 2; Length 167;			
Best Local Similarity		83.2%; Pred. No. 2.2e-45;			
Matches 84; Conservative		2; Mismatches 8; Indels 7; Gaps 1;			
Qy	1	REDDRLPLANIRIMKALPXXGKXXXXXIAKAKXKXQECVSEFISITSEASXKC 60			
Db	19	REDDRLPLANIRIMKALPANGK-----IAKAKETVQECVSEFISITSEASDKC 71			
Qy	61	QXERKTINGDDLLMAMATGTFEDYIEPLKYLXXYREXEG 101			
Db	72	QXERKTINGDDLLMAMATGTFEDYIEPLKYLXXYREXEG 112			
RESULT 2					
CBFA_MAIZ		STANDARD;	PRT;	179 AA.	
ID	P25209;				

DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE CCAAT-binding transcription factor subunit A (CBF-A) (NF-Y protein chain B) (NF-YB) (CAAT-box DNA binding protein subunit B).  
 GN Name=NFY2;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 NC NCBL\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92195809; PubMed=1549471;  
 RA Li X.-Y., Mantovani R., Hooft van Hujsdujnen R., Andre I.,  
 RA Benoit C., Mathis D.,  
 RT "Evolutionary variation of the CCAAT-binding transcription factor NF-  
 Y.";  
 RL Nucleic Acids Res. 20:1087-1091(1992).  
 CC -1- FUNCTION: Stimulates the transcription of various genes by  
 CC recognizing and binding to a CCAAT motif in promoters, for example  
 CC in type 1 collagen, albumin and beta-actin genes.  
 CC -1- SUBUNIT: Heterotrimeric transcription factor composed of three  
 CC components, A, B and C. NF-YB and NF-YC must interact and dimerize  
 CC for NF-YA association and DNA binding.  
 CC -1- DOMAIN: Can be divided into three domains: the weakly conserved A  
 CC domain, the highly conserved B domain thought to be involved in  
 CC subunit interaction and DNA binding, and the Glu-rich C domain.  
 CC -1- SIMILARITY: Belongs to the CBF-A subunit family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 CC EMBL: X59714, CAA42234.1, -.  
 DR FPI: 62820, 62820.  
 DR HSP: P25208, IN1J.  
 DR TRANSFAC: T05212, -.  
 DR MaizeDB: 69282, -.  
 DR InterPro: IPR003956, CBF\_A\_NFYB.  
 DR InterPro: IPR003958, CBF\_A\_NFYB\_domain.  
 DR InterPro: IPR003957, CBF\_A\_NFYB\_tople.  
 DR InterPro: IPR007124, Hist\_TAF.  
 DR InterPro: IPR009072, Histone-fold.  
 DR Pfam: PF00808, CBF\_NFYB\_HNF.1.  
 DR PRINTS: PR00615, COATSUBUNITA.  
 DR PROSITE: PS00685, CBF\_A\_NFYB.1.  
 KM Activator; DNA-binding; Nuclear protein; Transcription regulation.  
 FT DOMAIN 1 29 A domain.  
 FT DOMAIN 30 119 B domain.  
 FT DOMAIN 120 179 C domain.  
 FT DNA BIND 36 42 By similarity.  
 SO SEQUENCE 179 AA; 18995 MM; 3062316CEB69454 CRC64;  
 Query Match 91.0%; Score 417.5; DB 1; Length 179;  
 Best Local Similarity 83.2%; Pred. No. 2,4e-45;  
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REORRYPIANISIMKALPYNKXXXXXXIXAKAKXTQECVSEFISITSEASXKC 60  
 DB 30 REORRYPIANISIMKALPYNK-----IAKDKATYQECVSEFISITSEASDKC 82  
 QY 61 QXKRTKINGDDLLAMATGTFEDYIPKLYLXXVYREXEG 101  
 DB 83 QXKRTKINGDDLLAMATGTFEDYIPKLYLXXVYREXEG 123  
 RESULT 3

OS Zea mays  
 ID 09SLG0 PRELIMINARY; PRT; 141 AA.  
 AC 09SLG0, 023633.  
 DT 01-MAY-2000 (TREMBlRel. 13, Created)  
 DT 01-JUN-2002 (TREMBlRel. 21, Last sequence update)  
 DE CCAAT-binding transcription factor subunit A (Transcription factor).  
 GN Name=At2g38880; Synonyms=haptA;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 NC NCBL\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rounsaey S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,  
 RA Shen M., Roming C.M., Fraser C.M., Somerville C.R., Venter J.C.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Town C.D., Kaul S.,  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Edwards D., Smith A.G., Murray J.A.,  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.U., Volfovsky N., Town C.D., Tronkhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.,  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation." J.3:RESEARCH0029-RESEARCH0029 (2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Tronkhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.,  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M.,  
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
 RA Southwick A., Topp M.G., Wu T., Shinzaki K., Davis R.W., Ecker J.R.,  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M.,  
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
 RA Southwick A., Topp M.G., Wu T., Shinzaki K., Davis R.W., Ecker J.R.,  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y13723, CAA74051.1, -.  
 DR EMBL: Y13723, CAA74051.1, -.  
 DR EMBL: BT004286, AAC42288.1, -.  
 DR EMBL: BT005536, AAC63956.1, -.  
 DR PIR: B84810, B84810.  
 DR HSP: P25208, IN1J.  
 DR TRANSFAC: T05198, -.  
 DR ANT-2DPAGE: 09SLG0, -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956, CBF\_A\_NFYB.

DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB\_topis.  
 DR InterPro: IPR003072; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB.1.  
 SQ SEQUENCE 141 AA; 15181 MW; D33060B5MD21D9E0 CRC64;

Query Match 90.3%; Score 414.5; DB 2; Length 141;  
 Best Local Similarity 81.2%; Pred. No. 4.5e-45;  
 Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTXQECVSEFISFITSBAAXKC 60  
 Db 20 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSBAADKC 72  
 Qy 61 QXERKKTNGDDLAMATLGFEDYIEPLKYILXXYREXEG 101  
 Db 73 QXERKKTNGDDLAMATLGFEDYIEPLKYILARYELEG 113

RESULT 4  
 067XJ2 PRELIMINARY; PRT; 176 AA.

AC 067XJ2; 28-0CT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Transcription factor NF-Y, CCAAT-binding-like protein.  
 GN Name:At3G53340;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Totsuki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamuya A.,  
 RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.,  
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs";  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AKL76827; BAD44590.1; -  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB\_topis.  
 DR InterPro: IPR003957; CBFA\_NFYB\_domain.  
 DR InterPro: IPR003972; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB.1.  
 SQ SEQUENCE 176 AA; 19155 MW; 7F26X068342ED485 CRC64;

Query Match 88.8%; Score 407.5; DB 2; Length 176;  
 Best Local Similarity 80.2%; Pred. No. 4.5e-44;  
 Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTXQECVSEFISFITSBAAXKC 60  
 Db 28 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSBAADKC 80  
 Qy 61 QXERKKTNGDDLAMATLGFEDYIEPLKYILXXYREXEG 101  
 Db 81 QXERKKTNGDDLAMATLGFEDYIEPLKYILARYELEG 121

RESULT 5  
 09LF13 PRELIMINARY; PRT; 228 AA.  
 AC 09LF13;

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transcription factor NF-Y, CCAAT-binding-like protein.  
 GN Name:At4P12.40;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bioecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,  
 RA Salanoubat M.,  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: ALI32966; CAB67641.1; -  
 DR PIR: T45874; T45874.  
 DR HSPP: P25208; IN1J.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB\_domain.  
 DR InterPro: IPR003957; CBFA\_NFYB\_topis.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB.1.  
 SQ SEQUENCE 228 AA; 25132 MW; BC158A80A08579B6 CRC64;

Query Match 88.8%; Score 407.5; DB 2; Length 228;  
 Best Local Similarity 80.2%; Pred. No. 5.9e-44;  
 Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTXQECVSEFISFITSBAAXKC 60  
 Db 28 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSBAADKC 80  
 Qy 61 QXERKKTNGDDLAMATLGFEDYIEPLKYILXXYREXEG 101  
 Db 81 QXERKKTNGDDLAMATLGFEDYIEPLKYILARYELEG 121

RESULT 6

AC 08VYK4 PRELIMINARY; PRT; 173 AA.  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 03-JUN-2004 (TREMBlrel. 27, Last annotation update)  
 DE At2g37060/T2N18.18.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlín-Neumann G.,  
 RA Kawai J., Lam B., Lee J.W., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.,  
 RL Submitted (BNC-2001) to the EMBL/GenBank/DBJ databases.

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTXQECVSEFISFITSBAAXKC 60  
 Db 28 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSBAADKC 80  
 Qy 61 QXERKKTNGDDLAMATLGFEDYIEPLKYILXXYREXEG 101  
 Db 81 QXERKKTNGDDLAMATLGFEDYIEPLKYILARYELEG 121

RP SEQUENCE FROM N.A.  
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
 RA Bower L., Carninci P., Chang B., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin U., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.,  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY070477; AA149943.1; -.  
 DR EMBL: AY091673; AA110272.1; -.  
 DR HSSP: P25208; INTJ.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB; 1.  
 SQ SEQUENCE 173 AA; 1898 MW; 8C01E135B2DEC36A CRC64;  
 Query Match 87.7%; Score 402.5; DB 2; Length 173;  
 Best Local Similarity 79.2%; Pred. No. 1.9e-43;  
 Matches 80; Conservative 4; Mismatches 10; Indels 7; Gaps 1;  
 QY 1 REODRYPLIANISIRIMKALPXNGKXXXXXXIXAKDAKTXQSCVSFISFISEASXKC 60  
 DB 29 REODRPLPIANISIRIMKALPXNGK-----IAKDAKTXQSCVSFISFISEASDKC 81  
 QY 61 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYLXXYREXEG 101  
 DB 82 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYLXXYREXEG 122  
 RESULT 7  
 ID 023310 PRELIMINARY; PRT; 161 AA.  
 AC 023310;  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE CCAAT-binding transcription factor subunit A (CBF-A) (Putative CCAAT-  
 binding transcription factor subunit A CBF-A) (At4g15450).  
 GN Name=dl3310w; Synonym=At4g15450; At4g15450/dl3310w;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_Taxid=3702;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Stelekema W., Murphy G., Wambutt R., Pohl T., Terry N.,  
 RA Kreis M., Kavanagh T., Ertter K.D., Rieger M., James R.,  
 RA Pridmore P., Hatzopoulos P., Obermaier B., Dueschopf A.,  
 RA Jones J., Palme K., Ansgore W., Delseny M., Bancroft I., Mewes H.W.,  
 RA Scheller C., Chalwatzis N.,  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.,  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.

RA Shinn P., Chen H., Cheuk R., Kim C.J., Bower L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Huan V.W.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin U., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z97336; CAB10233.1; -.  
 DR EMBL: AL161539; CAB78496.1; -.  
 DR EMBL: AK117818; BAC42460.1; -.  
 DR EMBL: BT003684; AAC039912.1; -.  
 DR PIR: G71407; G71407.  
 DR HSSP: P25208; INTJ.  
 DR TRANSFAC: T05340; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1s.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Histone-TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB; 1.  
 SQ SEQUENCE 161 AA; 17186 MW; 5C452E20D98A7AF4 CRC64;  
 Query Match 87.3%; Score 400.5; DB 2; Length 161;  
 Best Local Similarity 78.2%; Pred. No. 3.3e-43;  
 Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;  
 QY 1 REODRYPLIANISIRIMKALPXNGKXXXXXXIXAKDAKTXQSCVSFISFISEASXKC 60  
 DB 20 REODRPLPIANISIRIMKALPXNGK-----ISKDAKTXQSCVSFISFISEASDKC 72  
 QY 61 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYLXXYREXEG 101  
 DB 73 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYLXXYREXEG 113  
 RESULT 8  
 ID 023634 PRELIMINARY; PRT; 187 AA.  
 AC 023634;  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transcription factor (Fragment).  
 GN Name=hap3b;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_Taxid=3702;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Edwards D., Smith A.G., Murray J.A.,  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y13724; CAA74052.1; -.  
 DR HSSP: P25208; INTJ.  
 DR TRANSFAC: T05195; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1s.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Histone-TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB; 1.

PT NON TER 1 1  
SQ SEQUENCE 187 AA; 20295 MW; EAC7ABC89F37F408 CRC64;  
Query Match 86.2%; Score 395.5; DB 2; Length 187;  
Best Local Similarity 76.2%; Pred. No. 1.7e-42;  
Matches 77; Conservative 6; Mismatches 11; Indels 7; Gaps 1;  
Qy 1 REODRYPINANISIRIMKALPXNGKXXXXXXIAKDANKTXQECVSEFISFITSASXKC 60  
Db 23 REODRFLPIANVNSIRIMKALPXNPK-----ISKDAETWQECVSEFISFITSASXKC 75  
Qy 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKYLLXXYREXG 101  
Db 76 QXERKRTINGDDLLMAMATLGFEDYIEPLKYLLQRFREIEG 116  
RESULT 9  
Q9FGJ3 PRELIMINARY; PRT; 190 AA.  
AC Q9FGJ3;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DE Similarity to COAT-box-binding transcription factor  
DE (AT5947640/MN7.23).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_Taxid=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kaneke T., Katon T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RA Tabata S.; (APR-1999) to the EMBL/GenBank/DBJ databases.  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,  
RA Carinci P., Chang B., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Shih P., Chen H., Cheuk R., Kim C.J., Koesema B., Meyers M.C.,  
RA Tracy S.E., Banh J., Bowser L., Carinci P., Chung M.K.,  
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,  
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,  
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,  
RA Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA EMBL; AB025628; BAB09090.1; -  
DR EMBL; AY078026; AAL7727.1; -  
DR EMBL; AF385744; AAK60334.1; -  
DR HSSP; P25208; 1N1J.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; P:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR003958; CBFA\_NFYB domain.  
DR InterPro; IPR003957; CBFA\_NFYB top1.  
DR InterPro; IPR009072; Histone-fold.  
DR InterPro; IPR007124; Hist. TAR.  
DR Pfam; PF00808; CBFD\_NFYB\_HMF; 1.  
DR PRINTS; PR00615; CCAATSUBNTA.  
DR PROSITE; PS00685; CBFA\_NFYB; 1.  
SQ SEQUENCE 190 AA; 20529 MW; DBSCFOP42247C02 CRC64;

Query Match 86.2%; Score 395.5; DB 2; Length 190;  
Best Local Similarity 76.2%; Pred. No. 1.7e-42;  
Matches 77; Conservative 6; Mismatches 11; Indels 7; Gaps 1;  
Qy 1 REODRYPINANISIRIMKALPXNGKXXXXXXIAKDANKTXQECVSEFISFITSASXKC 60  
Db 26 REODRFLPIANVNSIRIMKALPXNPK-----ISKDAETWQECVSEFISFITSASXKC 78  
Qy 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKYLLXXYREXG 101  
Db 79 QXERKRTINGDDLLMAMATLGFEDYIEPLKYLLQRFREIEG 119  
RESULT 10  
Q9ZOC3 PRELIMINARY; PRT; 178 AA.  
AC Q9ZOC3;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DE Similarity to COAT-box binding transcription factor.  
DE Putative COAT-box binding transcription factor.  
GN Name=At2g37060;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_Taxid=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanKen S.B.,  
RA Barnstead M.B., Mason T.M., Bowman C.L., Roming C.M., Bentto M.-I.,  
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
RA Fraser C.M., Venter J.C.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Town C.D., Kaul S.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA EMBL; AC006260; AAD18153.1; -  
DR PIR; A84788; A84788.  
DR HSSP; P25208; 1N1J.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; P:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR003958; CBFA\_NFYB domain.  
DR InterPro; IPR003957; CBFA\_NFYB top1.  
DR InterPro; IPR009072; Histone-fold.  
DR InterPro; IPR007124; Hist. TAR.  
DR Pfam; PF00808; CBFD\_NFYB\_HMF; 1.  
DR PRINTS; PR00615; CCAATSUBNTA.  
DR PROSITE; PS00685; CBFA\_NFYB; 1.  
SQ SEQUENCE 178 AA; 19523 MW; B3CF497383EC86C4 CRC64;  
Query Match 85.7%; Score 393.5; DB 2; Length 178;  
Best Local Similarity 76.0%; Pred. No. 2.9e-42;  
Matches 78; Conservative 5; Mismatches 10; Indels 7; Gaps 1;  
Qy 1 REODRYPINANISIRIMKALPXNGKXXXXXXIAKDANKTXQECVSEFISFITSASXKC 60  
Db 29 REODRFLPIANVNSIRIMKALPXNPK-----ISKDAETWQECVSEFISFITSASXKC 81  
Qy 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKYLLXXYREXG 100  
Db 82 QXERKRTINGDDLLMAMATLGFEDYIEPLKYLLQRFREIEG 121  
RESULT 11  
Q84VF3 PRELIMINARY; PRT; 152 AA.  
AC Q84VF3;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE CCAAT-binding transcription factor-like protein (Fragment).  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 ON NCBI\_Taxid=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2311120; PubMed=14750518;  
 RX DOI=10.1023/B:PAM.000007001.30865.0f;  
 RA Cooper B., Hutchison D., Park S., Guimil S., Lugimbuhl P., Ellero C.,  
 RA Goff S.A., Glazebrook J.;  
 RT "Identification of rice (*Oryza sativa*) proteins linked to the cyclin-  
 RT mediated regulation of the cell cycle.";  
 RL Plant Mol. Biol. 53:273-279(2003).  
 DR EMBL: AY224530; AAO72650.1; -.  
 DR HSSP: P25208; 1MJT.  
 DR Gramene; Q84VF3; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1s.  
 DR InterPro: IPR007124; Histone-fold.  
 DR InterPro: IPR007124; Histone-fold.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
 DR PRINTS; PR00615; CCAATSUBUNTA.  
 DR PROSITE; PS00685; CBFA\_NFYB; 1.  
 FT NON TER 1  
 SQ SEQUENCE 152 AA; 16456 MW; 89EB826AD6124EFB CRC64;  
 Query Match 84.6%; Score 388.5; DB 2; Length 152;  
 Best Local Similarity 83.2%; Pred. No. 1.1e-41;  
 Matches 79; Conservative 1; Mismatches 8; Indels 7; Gaps 1;  
 QY 7 LPIANISRIKMKALPXNGKXXXXXXIAKDAKXTQCVSEFISFITSASXKCQXKRRK 66  
 DB 10 LPIANISRIKMKALPXNGK-----IAKDAKXTQCVSEFISFITSASXKCQXKRRK 62  
 QY 67 TINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
 DB 63 TINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 97  
 RESULT 12  
 ID Q84NFI PRELIMINARY; PRT; 178 AA.  
 AC Q84NFI;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE HAP3.  
 GN Name=OSHAP3A;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 ON NCBI\_Taxid=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22983257; PubMed=14617083;  
 RX DOI=10.1023/B:PAM.000007001.30865.0f;  
 RA Miyoshi K., Ito Y., Serizawa A., Kurata N.;  
 RA "OSHAP3 genes regulate chloroplast biogenesis in rice.";  
 RL Plant J. 36:532-540(2003).  
 DR EMBL: AB095438; BAC76331.1; -.  
 DR HSSP: P25208; 1MJT.  
 DR Gramene; Q84NFI; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0006377; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.

DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1s.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Histone-fold.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
 DR PRINTS; PR00615; CCAATSUBUNTA.  
 DR PROSITE; PS00685; CBFA\_NFYB; 1.  
 SQ SEQUENCE 178 AA; 19200 MW; 1D620383B9E82926 CRC64;  
 Query Match 84.6%; Score 388.5; DB 2; Length 178;  
 Best Local Similarity 75.2%; Pred. No. 1.3e-41;  
 Matches 76; Conservative 9; Mismatches 9; Indels 7; Gaps 1;  
 QY 1 REODRYLPIANISRIKMKALPXNGKXXXXXXIAKDAKXTQCVSEFISFITSASXKC 60  
 DB 33 REODRYLPIANISRIKMKALPXNGK-----IAKDAKXTQCVSEFISFITSASXKC 85  
 QY 61 QXKERTINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
 DB 86 QXKERTINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 126  
 RESULT 13  
 ID Q851T8 PRELIMINARY; PRT; 189 AA.  
 AC Q851T8;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Putative CAAT-box DNA binding protein (CCAAT-binding protein).  
 GN Name=PO506B12.4; Synonym=CCB1, P0460C04.24;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 ON NCBI\_Taxid=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12447436; DOI=10.1038/nature01184;  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Karamori H.,  
 RA Hosokawa S., Masukawa M., Arikawa K., Chien Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijiwhara S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh Y., Itoh Y., Itoh Y., Iwabuuchi A., Kamuya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Yama H., Endo T., Ito H., Hahn J.H., Kim H.I., Sun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yao Q., Peng R., Xiong A.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP003271; BAB89732.1; -.  
 DR EMBL: AP004366; BAB92931.1; -.  
 DR EMBL: AY32466; AAO01152.1; -.  
 DR HSSP: P25208; 1MJT.  
 DR Gramene; Q851T8; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0006377; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1s.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Histone-fold.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.



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DR PRINTS; PRO0615; CCAATSUBUNTA.
DR PROSITE; PS00685; CBFA_NFYB; 1. 0D385703DAC25D3 CRC64;
SQ SEQUENCE 189 AA; 20752 MW; 1.4e-41;

Query Match 84.6%; Score 388.5; DB 2; Length 189;
Best Local Similarity 75.2%; Pred. No. 1.4e-41;
Matches 76; Conservative 9; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYPIANISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60
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DB 19 REODRFLPIANVSRIMKALPANAK-----ISKDAKETVQECVSEFISFITSASDKC 71
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 QXERKRTINGDDLLMAMATLGFEDYIRPLKVTLYXXYREXEG 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 72 QXERKRTINGEDLLPMAGTIGFEDYVDP LKYLHKFRFLEEG 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
ID Q69J40 PRELIMINARY; PRT; 224 AA.
AC Q69J40;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Putative transcription factor.
GN Name=OSUNBA0072106.11; Synonyms=P0493C06.26;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;

RN [1]
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nupponbare (GA3) genomic DNA, chromosome 7, BAC
   clone:OSUNBA0072106.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RN [2]
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nupponbare (GA3) genomic DNA, chromosome 7, PAC
   clone:P0493C06.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP006458; BAD32022.1; -.
DR EMBL; AP005193; BAD31143.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003956; CBFA_NFYB.
DR InterPro; IPR003958; CBFA_NFYB_domain.
DR InterPro; IPR003957; CBFA_NFYB_topls.
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR007124; Hist_TAF.
DR Pfam; PF00808; CBFD_NFYB_HMF.1.
DR PRINTS; PRO0615; CCAATSUBUNTA.
DR PROSITE; PS00685; CBFA_NFYB; 1.
SQ SEQUENCE 224 AA; 23273 MW; D2E32DC64D138BFF CRC64;

Query Match 84.6%; Score 388.5; DB 2; Length 224;
Best Local Similarity 75.2%; Pred. No. 1.6e-41;
Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

QY 1 REODRYPIANISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 21 REODRFLPIANVSRIMKALPANAK-----ISKDAKETVQECVSEFISFITSASDKC 73
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 QXERKRTINGDDLLMAMATLGFEDYIRPLKVTLYXXYREXEG 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 74 QXERKRTINGDDLLMAMATLGFEDYVDP LKYLHKFRFLEEG 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
Q6YMK1

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ID Q6YMK1 PRELIMINARY; PRT; 219 AA.
AC Q6YMK1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE HAP3-like transcriptional-activator.
GN Name=HAP3;
OS Oryza sativa (Indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=39946;

RN [1]
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nupponbare (GA3) genomic DNA, chromosome 7, BAC
   clone:OSUNBA0072106.11; Synonyms=P0493C06.26;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY062181; AAL47206.1; -.
DR HSRP; P19267.1A7W.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003956; CBFA_NFYB.
DR InterPro; IPR003958; CBFA_NFYB_domain.
DR InterPro; IPR003957; CBFA_NFYB_topls.
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR007124; Hist_TAF.
DR Pfam; PF00808; CBFD_NFYB_HMF.1.
DR PRINTS; PRO0615; CCAATSUBUNTA.
DR PROSITE; PS00685; CBFA_NFYB; 1.
SQ SEQUENCE 219 AA; 22987 MW; 704BD8B9E0C5F2C0 CRC64;

Query Match 84.2%; Score 386.5; DB 2; Length 219;
Best Local Similarity 75.2%; Pred. No. 2.9e-41;
Matches 76; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 REODRYPIANISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 23 REODRFLPIANVSRIMKALPANAK-----ISKDAKETVQECVSEFISFITSASDKC 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 QXERKRTINGDDLLMAMATLGFEDYIRPLKVTLYXXYREXEG 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 76 QXERKRTINGDDLLMAMATLGFEDYVDP LKYLHKFRFLEEG 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 17, 2005, 08:55:33
Job time : 170 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:46:10 ; Search time 25 Seconds  
(Without alignments)  
301.582 Million cell updates/sec

Title: US-10-678-588A-8

Perfect score: 459  
Sequence: 1 REDDRYLPANIRIMKAL.....FEDYIRPKYLYKXREXEG 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A COMB pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B COMB pep.\*  
3: /cgn2\_6/prodata/1/1aa/6A COMB pep.\*  
4: /cgn2\_6/prodata/1/1aa/6B COMB pep.\*  
5: /cgn2\_6/prodata/1/1aa/PCUS COMB pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfile1 pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402.5	87.7	90	3 US-09-103-478-20	Sequence 20, Appl
2	402.5	87.7	90	3 US-09-193-931C-20	Sequence 20, Appl
3	402.5	87.7	90	4 US-09-516-052-30	Sequence 30, Appl
4	401.5	86.6	218	4 US-09-828-303-23	Sequence 23, Appl
5	397.5	86.6	219	4 US-09-640-211A-1051	Sequence 1051, Ap
6	337.5	73.5	207	4 US-09-538-092-1008	Sequence 1008, Ap
7	337.5	73.5	211	4 US-09-949-016-7348	Sequence 7348, Ap
8	332.5	72.4	90	3 US-09-103-478-21	Sequence 21, Appl
9	332.5	72.4	90	3 US-09-103-478-24	Sequence 24, Appl
10	332.5	72.4	90	3 US-09-103-478-25	Sequence 25, Appl
11	332.5	72.4	90	3 US-09-193-931C-21	Sequence 21, Appl
12	332.5	72.4	90	3 US-09-193-931C-24	Sequence 24, Appl
13	332.5	72.4	90	3 US-09-193-931C-25	Sequence 25, Appl
14	332.5	72.4	90	4 US-09-516-052-31	Sequence 31, Appl
15	332.5	72.4	90	4 US-09-516-052-34	Sequence 34, Appl
16	332.5	72.4	90	4 US-09-516-052-35	Sequence 35, Appl
17	331.5	72.2	90	3 US-09-103-478-22	Sequence 22, Appl
18	331.5	72.2	90	3 US-09-193-931C-22	Sequence 22, Appl
19	331.5	72.2	90	4 US-09-516-052-32	Sequence 32, Appl
20	329.5	71.8	90	3 US-09-103-478-26	Sequence 26, Appl
21	329.5	71.8	90	3 US-09-193-931C-26	Sequence 26, Appl
22	329.5	71.8	90	4 US-09-516-052-36	Sequence 36, Appl
23	323.5	70.5	146	4 US-09-435-054A-8	Sequence 8, Appl1
24	323.5	70.5	240	4 US-09-435-054A-10	Sequence 10, Appl
25	323.5	70.3	355	4 US-09-435-054A-18	Sequence 18, Appl
26	322.5	70.3	214	4 US-09-435-054A-12	Sequence 12, Appl
27	319.5	69.6	205	4 US-09-516-052-20	Sequence 20, Appl

## ALIGNMENTS

28	319.5	69.6	216	4 US-09-516-052-22	Sequence 22, Appl
29	317.5	69.2	108	4 US-09-640-211A-1174	Sequence 1174, Ap
30	316.5	69.0	278	4 US-09-435-054A-2	Sequence 2, Appl1
31	315.5	68.7	109	4 US-09-248-796A-18639	Sequence 18639, A
32	308.5	67.2	208	3 US-09-103-478-2	Sequence 2, Appl1
33	308.5	67.2	208	3 US-09-193-931C-2	Sequence 2, Appl1
34	308.5	67.2	208	4 US-09-026-221-2	Sequence 2, Appl1
35	308.5	67.2	208	4 US-09-538-029-70	Sequence 70, Appl
36	308.5	67.2	208	4 US-09-516-052-2	Sequence 2, Appl1
37	307.5	67.0	171	4 US-09-435-054A-20	Sequence 20, Appl
38	299.5	65.3	90	3 US-09-103-478-19	Sequence 19, Appl
39	299.5	65.3	90	3 US-09-193-931C-19	Sequence 19, Appl
40	299.5	65.3	90	4 US-09-516-052-29	Sequence 29, Appl
41	294.5	64.2	121	4 US-09-270-767-59691	Sequence 59691, A
42	294.5	64.2	164	4 US-09-270-767-44270	Sequence 44270, A
43	288.5	62.9	108	4 US-09-640-211A-1090	Sequence 1090, Ap
44	288.5	62.9	144	3 US-09-319-989-4	Sequence 4, Appl1
45	288.5	62.9	144	4 US-09-538-092-15	Sequence 15, Appl

## RESULT 1

US-09-103-478-20  
Sequence 20, Application US/09103478  
Patent No. 6235975  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Onco, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,478  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,221  
FILING DATE: 19-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Blinhorst, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-20

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Query Match      87.7%; Score 402.5; DB 3; Length 90;
Best Local Similarity 83.5%; Pred. No. 3.9e-52;
Matches 81; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQCVSEFISFITSASXKC 60
DB 1 REODRFLPIANISIRIMKALIPANGK-----IAKDAKXTQCVSEFISFITSASDKC 53

QY 61 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYXXR 97
DB 54 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYOKR 90

RESULT 2
US-09-193-931C-20
; Sequence 20, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; FILE REFERENCE: 023070-077620
; CURRENT APPLICATION NUMBER: US/09/193,931C
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 09/026,221
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 08/804,534
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(90)
; OTHER INFORMATION: maize HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF) protein B domain homolog
; US-09-193-931C-20

Query Match      87.7%; Score 402.5; DB 3; Length 90;
Best Local Similarity 83.5%; Pred. No. 3.9e-52;
Matches 81; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQCVSEFISFITSASXKC 60
DB 1 REODRFLPIANISIRIMKALIPANGK-----IAKDAKXTQCVSEFISFITSASDKC 53

QY 61 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYXXR 97
DB 54 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYOKR 90

RESULT 3
US-09-516-052-30
; Sequence 30, Application US/09516052
; Patent No. 6781035
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohno, Masa-Aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: Bul, Anhthu
; APPLICANT: Khong, Raymond
; APPLICANT: The Regents of the University of California
```

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; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; FILE REFERENCE: 023070-077630US
; CURRENT APPLICATION NUMBER: US/09/516,052
; CURRENT FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 09/193,931
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 09/026,221
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 08/804,534
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(90)
; OTHER INFORMATION: maize HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF) protein B domain homolog
; US-09-516-052-30

Query Match      87.7%; Score 402.5; DB 4; Length 90;
Best Local Similarity 83.5%; Pred. No. 3.9e-52;
Matches 81; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQCVSEFISFITSASXKC 60
DB 1 REODRFLPIANISIRIMKALIPANGK-----IAKDAKXTQCVSEFISFITSASDKC 53

QY 61 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYXXR 97
DB 54 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYOKR 90

RESULT 4
US-09-828-303-23
; Sequence 23, Application US/09828303
; Patent No. 6677504
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNET, HANS J.
; APPLICANT: VAN THIESEN, NOCHA
; APPLICANT: CHEN, RUDYING
; TITLE OF INVENTION: TRANSCRIPTION FACTOR STRESS-RELATED PROTEINS AND
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0030
; CURRENT APPLICATION NUMBER: US/09/828,303
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-828-303-23

Query Match      87.5%; Score 401.5; DB 4; Length 218;
Best Local Similarity 78.2%; Pred. No. 1.7e-51;
Matches 79; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQCVSEFISFITSASXKC 60
DB 34 REODRFLPIANISIRIMKALIPSNK-----ISKDAKXTQCVSEFISFITSASDKC 86

QY 61 QXERKRTINGDDLLMAMATLGFEEDYIBPLKVIYLYXXREXEG 101
DB 87 QXERKRTINGDDLLMAMSTLGFEEDYVPLKVIYLYHRYELEEG 127
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RESULT 5
US-09-640-211A-1051
; Sequence 1051, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modifications of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; PRIORITY FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1051
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-640-211A-1051

Query Match      86.6%; Score 397.5; DB 4; Length 219;
Best Local Similarity 75.2%; Pred. No. 6.8e-51;
Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60
Db 24 KEDRPLPIANVAGIMKALPANCK-----VSKDKETVQECVSEFISFITSASDKC 76
Qy 61 QXERKTINGDDILMAMATIGFEDYIEPLKYLYLXXYRE 101
Db 77 QXERKTINGDDILMAMATIGFEDYIEPLKYLYLXXYREMEG 117

RESULT 6
US-09-538-092-1008
; Sequence 1008, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIORITY FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1008
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P35208
US-09-538-092-1008

Query Match      73.5%; Score 337.5; DB 4; Length 207;
Best Local Similarity 67.3%; Pred. No. 5.5e-42;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60
Db 53 REODIYLPINAVARIMKALPQTK-----IAKDAKCVQECVSEFISFITSASERC 105
Qy 61 QXERKTINGDDILMAMATIGFEDYIEPLKYLYLXXYRE 98

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Db 106 HQERKTINGEDILFAMSTIGFDSYVEPLKYLYLQKPRE 143

RESULT 7
US-09-949-016-7348
; Sequence 7348, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7348
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7348

Query Match      73.5%; Score 337.5; DB 4; Length 211;
Best Local Similarity 67.3%; Pred. No. 5.7e-42;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQECVSEFISFITSASXKC 60
Db 56 REODIYLPINAVARIMKALPQTK-----IAKDAKCVQECVSEFISFITSASERC 108
Qy 61 QXERKTINGDDILMAMATIGFEDYIEPLKYLYLXXYRE 98
Db 109 HQERKTINGEDILFAMSTIGFDSYVEPLKYLYLQKPRE 146

RESULT 8
US-09-103-478-21
; Sequence 21, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-21

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1,1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRINKALPKNKXXXXXXXXXAKDAKXTXQCVSEFFISFITSASXKC 60  
Db 1 REODIYLPINVARIMKNAIPQTGK-----IAKDAKECVQCVSEFFISFITSASERC 53

Qy 61 QXERKRTINGDDILMAMATIGFEDYIBPLKVIYLYXXR 97  
Db 54 HQERKRTINGEDILFAMSTIGFQSYVEPLKVIYLYQKFR 90

## RESULT 9

US-09-103-478-24  
Sequence 24, Application US/09103478  
Patent No. 6235975  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohno, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,478  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,221  
FILING DATE: 19-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-24

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1,1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRINKALPKNKXXXXXXXXXAKDAKXTXQCVSEFFISFITSASXKC 60  
Db 1 REODIYLPINVARIMKNAIPQTGK-----IAKDAKECVQCVSEFFISFITSASERC 53

Qy 61 QXERKRTINGDDILMAMATIGFEDYIBPLKVIYLYXXR 97  
Db 54 HQERKRTINGEDILFAMSTIGFQSYVEPLKVIYLYQKFR 90

## RESULT 10

US-09-103-478-25  
Sequence 25, Application US/09103478  
Patent No. 6235975  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohno, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,478  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,221  
FILING DATE: 19-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-25

Query Match 72.4%; Score 332.5; DB 3; Length 90;

Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPININISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINAVARIMGNALPQTGK-----IAKDAKECVQECVSEFISFITSASBRC 53

QY 61 QXERKRTINGDDLLMAMATIGFEDYIRPLKVIKXXR 97  
Db 54 HOERKRTINGEDILFAMSTIGFOSYVEPLKVILOKFR 90

RESULT 11  
US-09-193-931C-21  
Sequence 21, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C  
CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Gallus sp.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: chicken HAP3 subunit of CCAAT box-binding factor  
US-09-193-931C-21

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPININISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINAVARIMGNALPQTGK-----IAKDAKECVQECVSEFISFITSASBRC 53  
QY 61 QXERKRTINGDDLLMAMATIGFEDYIRPLKVIKXXR 97  
Db 54 HOERKRTINGEDILFAMSTIGFOSYVEPLKVILOKFR 90

RESULT 12  
US-09-193-931C-24  
Sequence 24, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C

CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: human HAP3 subunit of CCAAT box-binding factor  
US-09-193-931C-24

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPININISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINAVARIMGNALPQTGK-----IAKDAKECVQECVSEFISFITSASBRC 53  
QY 61 QXERKRTINGDDLLMAMATIGFEDYIRPLKVIKXXR 97  
Db 54 HOERKRTINGEDILFAMSTIGFOSYVEPLKVILOKFR 90

RESULT 13  
US-09-193-931C-25  
Sequence 25, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C  
CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 25  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Mus musculus and Rattus norvegicus  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: mouse/rat HAP3 subunit of CCAAT box-binding factor  
US-09-193-931C-25

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPININISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINAVARIMGNALPQTGK-----IAKDAKECVQECVSEFISFITSASBRC 53

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Db      54 HOEKRKTNGEDILFPAMSTLGFQSIVPEPKLYLOKFR 90

RESULT 14
US-09-516-052-31
; Sequence 31, Application US/09516052
; Patent No. 6781035
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohno, Masa-Aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: Bul, Anhtnu
; APPLICANT: Khong, Raymond
; TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-077630US
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 09/193,931
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 09/026,221
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 90
TYPE: PRT
ORGANISM: Gallus sp.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(90)
OTHER INFORMATION: chicken HAP3 subunit of CCAAT box-binding factor
US-09-516-052-31

Query Match          72.4% Score 332.5; DB 4; Length 90;
Best Local Similarity 67.0%; Pred. No. 1.1e-41;
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1

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Db      54 HOEKRKTNGEDILFPAMSTLGFQSIVPEPKLYLOKFR 90

RESULT 15
US-09-516-052-34
; Sequence 34, Application US/09516052
; Patent No. 6781035
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohno, Masa-Aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: Bul, Anhtnu
; APPLICANT: Khong, Raymond
; TITLE OF INVENTION: LEAFY COTYLEDOMI Genes and their Uses
FILE REFERENCE: 023070-077630US

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CURRENT APPLICATION NUMBER: US/09/516,052
CURRENT FILING DATE: 2000-03-01
PRIORITY APPLICATION NUMBER: US 09/193,931
PRIORITY FILING DATE: 1998-11-17
PRIORITY APPLICATION NUMBER: US 09/103,478
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 09/026,221
PRIORITY FILING DATE: 1998-02-19
PRIORITY APPLICATION NUMBER: US 08/804,534
PRIORITY FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 90
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (1)..(90)
OTHER INFORMATION: human HAP3 subunit of CCAAT Box-binding factor
OTHER INFORMATION: (CBF) protein B domain homolog
US-09-516-052-34

Query Match          72.4%; Score 332.5; DB 4; Length 90;
Best Local Similarity 67.0%; Pred. No. 1,1e-41;
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1

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DB      1 REQRIYLPFPIANVARIMKVAIPQTGK-----IAKDAKECVQECVSEFISFITSASERC 53
QY      61 QXKRKTINGDILLAMATLGFEDYIEPLTKYILXXYR 97
DB      54 HQBRKTINGSDILLFAMSTLGFQSYVEPLKYLQKFR 90

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Search completed: November 17, 2005, 08:56:02  
Job time : 26 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:52:50 / Search time 165 Seconds

(without alignments)  
256.117 Million cell updates/sec

Title: US-10-678-588A-8

Perfect score: 459

Sequence: 1 REGDRIPLINIRIMKAL.....FEDYIEPLKYLXXREXEG 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
Published Applications AA:\*

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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	429	93.5	101	17	US-10-678-588A-8
2	425	92.6	185	17	US-10-678-588A-2
3	425	92.6	185	17	US-10-675-852-42
4	423.5	92.3	160	15	US-10-374-780A-802
5	423.5	92.3	160	17	US-10-675-852-26
6	423.5	92.3	173	15	US-10-424-599-274836
7	423.5	92.3	173	17	US-10-678-588A-6
8	423.5	92.3	173	17	US-10-675-852-24
9	423.5	92.3	174	15	US-10-424-599-274840
10	423.5	92.3	174	15	US-10-425-114-39733
11	423.5	92.3	174	17	US-10-675-852-84

12	423.5	92.3	185	15	US-10-425-114-48992	Sequence 48992, A
13	420.5	91.6	171	16	US-10-739-930-9314	Sequence 9314, Ap
14	420.5	91.6	176	17	US-10-675-852-64	Sequence 64, Appl
15	417.5	91.0	171	15	US-10-424-599-195353	Sequence 195353,
16	417.5	91.0	171	17	US-10-675-852-12	Sequence 12, Appl
17	417.5	91.0	178	14	US-10-180-375-197	Sequence 197, App
18	417.5	91.0	178	15	US-10-183-687-413	Sequence 413, App
19	417.5	91.0	178	15	US-10-374-780A-785	Sequence 785, App
20	417.5	91.0	178	15	US-10-399-883-32	Sequence 32, Appl
21	417.5	91.0	178	17	US-10-678-588A-3	Sequence 3, Appl1
22	417.5	91.0	178	17	US-10-675-852-46	Sequence 46, Appl
23	417.5	91.0	179	15	US-10-374-780A-786	Sequence 786, App
24	417.5	91.0	183	17	US-10-675-852-56	Sequence 56, Appl
25	417.5	91.0	188	17	US-10-675-852-38	Sequence 38, Appl
26	417.5	91.0	234	14	US-10-425-114-58164	Sequence 58164, A
27	414.5	90.3	141	15	US-10-112-887-2	Sequence 2, Appl1
28	414.5	90.3	141	15	US-10-225-068-114	Sequence 114, App
29	414.5	90.3	141	15	US-10-374-780A-88	Sequence 88, Appl
30	414.5	90.3	141	15	US-10-412-6998-1782	Sequence 1782, Ap
31	414.5	90.3	141	17	US-10-678-588A-7	Sequence 7, Appl1
32	414.5	90.3	141	17	US-10-675-852-2	Sequence 2, Appl1
33	414.5	90.3	141	17	US-10-225-068-114	Sequence 114, App
34	414.5	90.3	141	20	US-11-069-255-2	Sequence 2, Appl1
35	414.5	90.3	179	17	US-10-675-852-60	Sequence 60, Appl
36	414.5	90.3	182	14	US-10-180-375-174	Sequence 174, App
37	414.5	90.3	182	15	US-10-183-687-304	Sequence 304, App
38	414.5	90.3	182	15	US-10-399-883-24	Sequence 24, Appl
39	413.5	90.1	177	14	US-10-180-375-154	Sequence 154, App
40	413.5	90.1	177	15	US-10-183-687-284	Sequence 284, App
41	413.5	90.1	177	15	US-10-399-883-4	Sequence 4, Appl1
42	412.5	89.9	215	15	US-10-374-780A-791	Sequence 791, App
43	409.5	89.2	174	14	US-10-180-375-152	Sequence 152, App
44	409.5	89.2	174	15	US-10-183-687-282	Sequence 282, App
45	409.5	89.2	174	15	US-10-399-883-2	Sequence 2, Appl1

# ALIGNMENTS

RESULT 1  
US-10-678-588A-8  
Sequence 8, Application US/10678588A  
Publication No. US2005022266A1  
GENERAL INFORMATION:  
APPLICANT: Wu, Jingtui  
TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants  
FILE REFERENCE: 38-21(52578)C  
CURRENT APPLICATION NUMBER: US/10/678,588A  
CURRENT FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,758  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: US 60/425,157  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: US 60/463,787  
PRIOR FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 8  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURES:  
OTHER INFORMATION: protein consensus sequence  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (22)-(122)  
OTHER INFORMATION: Xaa can be Ala or Pro  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (26)-(126)  
OTHER INFORMATION: Xaa can be Thr or none  
FEATURE:  
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/ LOCATION: (27)..(27)
/ OTHER INFORMATION: Xaa can be Ile or none
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/ LOCATION: (28)..(28)
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/ OTHER INFORMATION: Xaa can be Ala or none
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US-10-678-588a-8

Query Match      93.5%; Score 429; DB 17; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.3e-51;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXOCVSEFISFISSEASXKC 60

Qy 61 QXERKTINGDDLLMAMATIGFEDYTEPLKVTLYLXXYREXEG 101
Db 61 QXERKTINGDDLLMAMATIGFEDYTEPLKVTLYLXXYREXEG 101

RESULT 2
US-10-678-588a-2
; Sequence 2, Application US/10678588A
; Publication No. US20050022266A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jingrui
; TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants
; FILE REFERENCE: 38-21(52578)C
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/ CURRENT APPLICATION NUMBER: US/10/678,588A
/ CURRENT FILING DATE: 2003-10-02
/ PRIOR APPLICATION NUMBER: US 60/415,758
/ PRIOR FILING DATE: 2002-10-02
/ PRIOR APPLICATION NUMBER: US 60/425,157
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: US 60/463,787
/ PRIOR FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 185
/ TYPE: PRT
/ ORGANISM: Zea mays
US-10-678-588a-2

Query Match      92.6%; Score 425; DB 17; Length 185;
Best Local Similarity 83.2%; Pred. No. 4.7e-50;
Matches 84; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

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Db 30 REODRYLPINISIRIMKALPXNGKXTIPANGKIAKDAKXTXOCVSEFISFISSEASDKC 89

Qy 61 QXERKTINGDDLLMAMATIGFEDYTEPLKVTLYLXXYREXEG 101
Db 90 QXERKTINGDDLLMAMATIGFEDYTEPLKVTLYLQKXREMG 130

RESULT 3
US-10-675-852-42
; Sequence 42, Application US/10675852
; Publication No. US20050086718A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: KEDDIE, James S
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omalra
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RATCHFEE, Oliver
; APPLICANT: KUMIMOTO, Roderick
; APPLICANT: GUTTERSON, Neal
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
; FILE REFERENCE: MBI-0022CIP
; CURRENT APPLICATION NUMBER: US/10/675,852
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/166,228
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/197,899
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 60/227,439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 10/112,887
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 10/286,264
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 10/225,068
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 185
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Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKTXOCVSEFFISFITSASXKC 60  
DB 27 REODRYLPINISIRIMKALPPNGK-----IAKADKTMQECVSEFFISFITSASEKC 79  
QY 61 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
DB 80 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYAREAREAG 120

RESULT 6  
US-10-424-599-274836  
Sequence 274836, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 274836  
LENGTH: 173  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURES:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_90198C.1.pep  
US-10-424-599-274836

Query Match 92.3%; Score 423.5; DB 15; Length 173;  
Best Local Similarity 85.1%; Pred. No. 6.9e-50;  
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKTXOCVSEFFISFITSASXKC 60  
DB 26 REODRYLPINISIRIMKALPPNGK-----IAKADKTMQECVSEFFISFITSASEKC 78  
QY 61 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
DB 79 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYAREAREAG 119

RESULT 7  
US-10-678-588a-6  
Sequence 6, Application US/10678588a  
Publication No. US2005002266A1  
GENERAL INFORMATION:  
APPLICANT: Wu, Jingrui  
TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants  
FILE REFERENCE: 38-21(52578)C  
CURRENT APPLICATION NUMBER: US/10/678,588a  
CURRENT FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,758  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: US 60/425,157  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: US 60/463,787  
PRIOR FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6  
LENGTH: 173  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-678-588a-6

Query Match 92.3%; Score 423.5; DB 17; Length 173;  
Best Local Similarity 85.1%; Pred. No. 6.9e-50;  
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKTXOCVSEFFISFITSASXKC 60  
DB 26 REODRYLPINISIRIMKALPPNGK-----IAKADKTMQECVSEFFISFITSASEKC 78  
QY 61 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
DB 79 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYAREAREAG 119

RESULT 8  
US-10-675-852-24  
Sequence 24, Application US/10675852  
Publication No. US20050086718A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Heard, Jacqueline B  
APPLICANT: Keddie, James S  
APPLICANT: CRESLMAN, Robert A  
APPLICANT: PINEDA, Omaira  
APPLICANT: JIANG, Cai-Zhong  
APPLICANT: RATCLIFFE, Oliver  
APPLICANT: KUMIMOTO, Roderick  
APPLICANT: GUTTERSON, Neal  
APPLICANT: SHERMAN, Bradley K  
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS  
FILE REFERENCE: MBI-0022CIP  
CURRENT APPLICATION NUMBER: US/10/675,852  
CURRENT FILING DATE: 2003-09-30  
PRIOR APPLICATION NUMBER: 10/412,699  
PRIOR FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 60/125,814  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 60/166,228  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/197,899  
PRIOR FILING DATE: 2000-04-17  
PRIOR APPLICATION NUMBER: 60/227,439  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 10/112,887  
PRIOR FILING DATE: 2002-03-18  
PRIOR APPLICATION NUMBER: 10/286,264  
PRIOR FILING DATE: 2003-01-23  
PRIOR APPLICATION NUMBER: 10/225,068  
PRIOR FILING DATE: 2002-08-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 24  
LENGTH: 173  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURES:  
OTHER INFORMATION: G3471 GLYMA-28NOV01-CLUSTER4778\_1 polypeptide  
US-10-675-852-24

Query Match 92.3%; Score 423.5; DB 17; Length 173;  
Best Local Similarity 85.1%; Pred. No. 6.9e-50;  
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKTXOCVSEFFISFITSASXKC 60  
DB 26 REODRYLPINISIRIMKALPPNGK-----IAKADKTMQECVSEFFISFITSASEKC 78  
QY 61 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
DB 79 QXERKRTINGDDLMMAMATLGFEDYIEPLKVIYLYAREAREAG 119

RESULT 9

US-10-424-599-274840  
 ; Sequence 274840, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 274840  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_90200C.1.pep  
 US-10-424-599-274840

Query Match 92.3%; Score 423.5; DB 15; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 7e-50;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKXTXQCVSFFISFITSASXKC 60  
 DB 27 REODRYLPINISIRIMKALPXNGK-----IAKDAKDTMQCVSFFISFITSASEKC 79  
 QY 61 QXERKRTINGDDLLMAMATIGFEDYIEPLKVVYLYXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATIGFEDYIEPLKVVYLYARREAG 120

RESULT 10  
 US-10-425-114-39733  
 ; Sequence 39733, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaka, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 39733  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700677948\_FLI.pep  
 US-10-425-114-39733

Query Match 92.3%; Score 423.5; DB 15; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 7e-50;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKXTXQCVSFFISFITSASXKC 60  
 DB 27 REODRYLPINISIRIMKALPXNGK-----IAKDAKDTMQCVSFFISFITSASEKC 79  
 QY 61 QXERKRTINGDDLLMAMATIGFEDYIEPLKVVYLYXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATIGFEDYIEPLKVVYLYARREAG 120

RESULT 11  
 US-10-675-852-84  
 ; Sequence 84, Application US/10675852  
 ; Publication No. US20050086718A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mendel Biotechnology, Inc.  
 ; APPLICANT: Heard, Jacqueline E  
 ; APPLICANT: KEDDIE, James S  
 ; APPLICANT: CREELMAN, Robert A  
 ; APPLICANT: PINEDA, Omar A  
 ; APPLICANT: JIANG, Cai-Zhong  
 ; APPLICANT: RATCLIFFE, Oliver  
 ; APPLICANT: KUMIMOTO, Roderick  
 ; APPLICANT: GUTTERSON, Neal  
 ; APPLICANT: SHERMAN, Bradley K  
 ; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS  
 ; FILE REFERENCE: MBI-0022CIP  
 ; CURRENT APPLICATION NUMBER: US/10/675,852  
 ; CURRENT FILING DATE: 2003-09-30  
 ; PRIOR APPLICATION NUMBER: 10/412,699  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: 09/533,030  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: 60/125,814  
 ; PRIOR FILING DATE: 1999-03-23  
 ; PRIOR APPLICATION NUMBER: 09/713,994  
 ; PRIOR FILING DATE: 2000-11-16  
 ; PRIOR APPLICATION NUMBER: 60/166,228  
 ; PRIOR FILING DATE: 1999-11-17  
 ; PRIOR APPLICATION NUMBER: 60/197,899  
 ; PRIOR FILING DATE: 2000-04-17  
 ; PRIOR APPLICATION NUMBER: 60/227,439  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 10/112,887  
 ; PRIOR FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 10/286,264  
 ; PRIOR FILING DATE: 2003-01-23  
 ; PRIOR APPLICATION NUMBER: 10/225,068  
 ; PRIOR FILING DATE: 2002-08-09  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 84  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: G3477 polypeptide  
 US-10-675-852-84

Query Match 92.3%; Score 423.5; DB 17; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 7e-50;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXIAKDAKXTXQCVSFFISFITSASXKC 60  
 DB 27 REODRYLPINISIRIMKALPXNGK-----IAKDAKDTMQCVSFFISFITSASEKC 79  
 QY 61 QXERKRTINGDDLLMAMATIGFEDYIEPLKVVYLYXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATIGFEDYIEPLKVVYLYARREAG 120

RESULT 12  
 US-10-425-114-48992  
 ; Sequence 48992, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaka, Jack E

```

/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 48992
/ LENGTH: 185
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700554268_F1.1.pap
US-10-425-114-48992

Query Match          92.3%; Score 423.5; DB 15; Length 185;
Best Local Similarity 85.1%; Pred. No. 7.5e-50;
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQBCVSEFISFITSASXKC 60
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Db 38 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTQBCVSEFISFITSASXKC 90
    |||

Qy 61 QEKRTKINGDDLLMAMATGFEFDYIEPLKYLXXYREXEG 101
    |||
Db 91 QEKRTKINGDDLLMAMATGFEFDYIEPLKYLXXYREXEG 131
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RESULT 13
US-10-739-930-9314
/ Sequence 9314, Application US/10739930
/ Publication No. US20040216190A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
/ TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
/ FILE REFERENCE: 38-21(5317)B
/ CURRENT APPLICATION NUMBER: US/10/739,930
/ CURRENT FILING DATE: 2003-12-18
/ NUMBER OF SEQ ID NOS: 11088
/ SEQ ID NO 9314
/ LENGTH: 171
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: GUYMA-23APR03-C6781_1.p
US-10-739-930-9314

Query Match          91.6%; Score 420.5; DB 16; Length 171;
Best Local Similarity 83.2%; Pred. No. 1.8e-49;
Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQBCVSEFISFITSASXKC 60
    |||
Db 25 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTQBCVSEFISFITSASXKC 77
    |||

Qy 61 QEKRTKINGDDLLMAMATGFEFDYIEPLKYLXXYREXEG 101
    |||
Db 78 QEKRTKINGDDLLMAMATGFEFDYIEPLKYLXXYREXEG 118
    |||

RESULT 14
US-10-675-852-64
/ Sequence 64, Application US/10675852
/ Publication No. US20050086718A1
/ GENERAL INFORMATION:
/ APPLICANT: Mendel Biotechnology, Inc.
/ APPLICANT: HEARD, Jacqueline B
/ APPLICANT: KEDDIE, James S
/ APPLICANT: CREELMAN, Robert A
/ APPLICANT: PINEA, Omalra
/ APPLICANT: JIANG, Cai-Zhong
/ APPLICANT: RATCLIFFE, Oliver
```

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/ APPLICANT: KUMIMOTO, Roderick
/ APPLICANT: GUTTERSON, Neal
/ APPLICANT: SHERMAN, Bradley K
/ TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
/ FILE REFERENCE: MBI-0022CIP
/ CURRENT APPLICATION NUMBER: US/10/675,852
/ CURRENT FILING DATE: 2003-09-30
/ PRIOR APPLICATION NUMBER: 10/412,699
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 60/125,814
/ PRIOR FILING DATE: 1999-03-23
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 60/166,228
/ PRIOR FILING DATE: 1999-11-17
/ PRIOR APPLICATION NUMBER: 60/197,899
/ PRIOR FILING DATE: 2000-04-17
/ PRIOR APPLICATION NUMBER: 60/227,439
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 10/112,887
/ PRIOR FILING DATE: 2002-03-18
/ PRIOR APPLICATION NUMBER: 10/286,264
/ PRIOR FILING DATE: 2003-01-23
/ PRIOR APPLICATION NUMBER: 10/225,068
/ PRIOR FILING DATE: 2002-08-09
/ Remaining prior application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 64
/ LENGTH: 176
/ TYPE: PRT
/ ORGANISM: Lycopersicon esculentum
/ FEATURE:
/ OTHER INFORMATION: SGN-UNIGENE-46859 polypeptide
US-10-675-852-64

Query Match          91.6%; Score 420.5; DB 17; Length 176;
Best Local Similarity 84.2%; Pred. No. 1.8e-49;
Matches 85; Conservative 1; Mismatches 8; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQBCVSEFISFITSASXKC 60
    |||
Db 33 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTQBCVSEFISFITSASXKC 85
    |||

Qy 61 QEKRTKINGDDLLMAMATGFEFDYIEPLKYLXXYREXEG 101
    |||
Db 86 QEKRTKINGDDLLMAMATGFEFDYIEPLKYLXXYREXEG 126
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RESULT 15
US-10-424-599-195353
/ Sequence 195353, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J
/ APPLICANT: Zhou Yihua
/ APPLICANT: Kovalic, David K
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 195353
/ LENGTH: 171
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_18430C.1.pap
US-10-424-599-195353
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Query Match 91.0%; Score 417.5; DB 15; Length 171;  
Best Local Similarity 82.2%; Pred. No. 4.6e-49;  
Matches 83; Conservative 3; Mismatches 8; Indels 7; Gaps 1;

Qy	1	REODRYLPINISIRIMKKALPXNGKXXXXXXXXIAKDAKXTXQECVSEFISFTSEASXC	60
Db	25	REODRYLPINISIRIMKKALPXNGKXXXXXXXXIAKDAKXTXQECVSEFISFTSEASXC	60
Qy	61	QXERKKTINGDDLMAMATLGFEDYIEPLKYYLXXYREXEG	101
Db	78	QXERKKTINGDDLMAMATLGFEDYMDPLKIYLTTRYREMEG	118

Search completed: November 17, 2005, 09:02:28  
Job time : 166 secs

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